GENOTYPIC EVALUATION OF

TRIFOLIUM AMBIGUUM

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ABSTRACT

A number of morphological, floral, rhizome, root and herbage characteristics were studied in order to describe genetic variation and environmental responses in *T. ambiguum*. From each of six lines, 30 genotypes were clonally progagated into five diverse edaphic and altitudinal sites and grown for one season. Comparisons of growth and form were also made between *T. ambiguum*, *T. repens* cv. 'Grasslands Huia' and *Lotus pedunculatus* cv. 'Grasslands Maku'.

The polyploid lines were found to have larger leaves than the diploids while all the lines of *T. ambiguum* had larger leaves than did white clover. Tetraploid lines had longer petioles and were taller and more erect than the diploids or hexaploids. Floral initiation was found to become later as ploidy level increased but the tetraploid lines exhibited a very large variation in flowering date.

The cultivar Treeline was found to produce the most herbage under all conditions although not significantly more than cultivar Prairie or C.P.I. 57353. However, as nodulation was not studied it was not possible to determine whether variety differences were due to root nodulating ability or some other genetically determined parameter.

None of the *T. ambiguum* varieties produced as much herbage as cv. Huia or cv. Maku at any site. However, all the *T. ambiguum* lines performed relatively better under harsher conditions. Because a large proportion of *T. ambiguum* was below ground the best *T. ambiguum* line, cultivar Treeline, produced equivalent total plant dry weight to cv. Huia and cv. Maku at 1200 m. a.s.l., the high altitude site.

Cultivar Prairie was found to have the highest proportion of rhizomes to total plant mass but because cv. Treeline had higher total plant dry weight both cultivars produced equivalent mean rhizome dry weight. The number of rhizomes, number of daughter plants and rhizome dry weight were all highly correlated and these three characteristics showed similar trends among varieties. Rhizome length was found to increase with ploidy level, as did rhizome internode length. However, the number of nodes was found to be higher in the diploids than in the polyploids. Cultivar Treeline was found to have a high proportion of branching nodes on its rhizomes while C.P.I. 57353 and cv. Summit had the least.

Rhizome production was restricted in the Wakanui silt loam soil of high bulk density. However, herbage growth and rhizome branching was increased, probably because of the higher fertility.

It was shown using factor analysis on genotypic correlations, that rhizome characteristics and herbage yields were relatively independantly inherited. However, morphological characters tended to be related to herbage yields.

The polyploid varieties were found to be more genetically variable than the diploids. Broad sense heritabilities were calculated for all parameters measured, and in general, morphological characteristics had higher values than agronomic characteristics.

As the genetic variation within each line was higher than the variation among lines, it is apparent that selection within lines should result in the largest gains. Therefore, comparison of the mean performance of the presently highly variable lines is relatively uninformative. By

sacrificing some genetic diversity, large gains could be made in performance. It is suggested that cv. Prairie be used as the basis for selecting a highly rhizomatous cultivar while cv. Treeline could be used in the selection of a cultivar with higher herbage production suitable for high country conditions.

In a second trial, an established stand of cv. Treeline produced up to 13250 kg ha^{-1} for one season under good growing conditions. The management required to produce this amount of herbage was to irrigate and cut to ground level every two months. The growth rate was considerably depressed when cut monthly. It was also shown that root and rhizome yield reached 12600 kg ha^{-1}, indicating a massive reserve of assimilates, particularly useful for surviving periods of stress. Seed yields were found to be adequate, reaching levels equivalent to 500-700 kg ha^{-1}.

These results were discussed in relation to earlier observations on *T. ambiguum* by workers in Russia, Australia, U.S.A. and New Zealand. Suggestions were made for further genetic and agronomic testing.

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CHAPTER 1

INTRODUCTION

Massive scree slopes, erosion pavements and exposed subsoil horizons are a common feature of New Zealand's South Island high country east of the main divide. Such marked and widespread deterioration of mountain soils has prompted national concern (McCaskill, 1973).

Natural historians now consider that physical weathering and subsequent erosion has been taking place at an accelerated rate since the cold periods of the Pleistocene which ended 12,000 years ago. However, within the last 1,000 years the process of landscape deterioration has been greatly accelerated. Uncontrolled fires, both natural and lit by Polynesian moa hunters, were followed by widespread and deliberate burning for pastoral improvement by pioneer Europeans. These repeated fires were accompanied by increased browsing and trampling by introduced domestic and wild animals. This resulted in depletion of ground cover and exposure of topsoils to a severe physical environment. Consequently, rapid acceleration of soil erosion was combined with an existing high rate of rock wasting. Erosive forces removed the often shallow topsoils which contained most of the available plant nutrients. This process often exposed highly infertile and frequently incohesive subsoils and colluvial parent material. Under the combined forces of severe climate, site instability and soil infertility, natural recovery of the original beech forests could not occur allowing impoverished tussock grasslands to establish (Daly, 1973).

In an eroded condition, the land has a reduced value for man as well as having an increased propensity for accelerated erosion. Although much

has been written about these lands, only recently has any effort been made toward their rehabilitation. The first steps of retiring high erosion risk lands from pastoral use and the control of wild animal populations are being taken. However, where erosive forces have removed the topsoil and even subsoil, these measures alone are not enough to restore effective vegetative cover.

Experimental work designed to provide techniques to revegetate these eroded lands, preferably with economically useful species, is very recent (Holloway 1970, Dunbar and Adams 1972). As found by these and other workers, harsh climate, low nutrient status of the remaining soils and short growing seasons are the most important limitations making revegetation by native or introduced species a most difficult task. Chemical analyses have shown that the soils are very low in nitrogen, phosphorus, sulphur, most of the minor elements and some of the trace elements (Taylor and Pohlen 1968, Dunbar and Adams 1972). Deficiencies of these available nutrients may be severely limiting plant growth and hence their ability to establish and survive both frost heave and the effects of intense seasonal cold. The best possible way to combat these problems in revegetation is to build up the soil nitrogen status by introducing nitrogen fixing species.

Research has shown that various nitrogen fixing species may be useful for revegetation. Indications from experiments in Australia (Costin and Wimbush 1963, Bryant 1974) and New Zealand (Paljor 1973, Meares 1975, Nordmeyer pers. comm.) are that *Trifolium ambiguum* could be a suitable plant for this purpose, if well adapted cultivars could be developed.

Trifolium ambiguum is a rhizomatous perennial legume from the mountainous Caucasus region of Southern Russia, Turkey and Iran (Komarov, 1945). Forms of this species are adapted to short growing seasons, harsh

climates and to soils of low nutrient status. The species also offers some potential as a pasture legume in high country regions where white clover *(T. repens)* fails to persist. However, nitrogen fixation is not always efficient and herbage production is generally low when compared with white clover.

Much of the previous work on *T. ambiguum* has been the screening of both host and *Rhizobium* populations for compatibility and effectiveness of nodulation. In Australia, however, some very intense selection for effective nodulation has been carried out with several cultivars (Hely 1957, 1963, 1971, 1972, 1975, Zorin 1975, 1976a, 1976b, 1976c). Apart from selecting for consistent flowering and seed production other characteristics have been given scant attention. Consequently, the cultivars developed by the Australians are highly variable in most plant characteristics. To breed highly rhizomatous cultivars for revegetation purposes and herbage producing cultivars for pastoral purposes, other factors, apart from flowering, seed production and nitrogen fixation need to be considered.

In the present work the aim of the first experiment was to compare the performance of six lines of *T. ambiguum* and to determine the potential for selection within each line. As selection response is dependent on the heritability and genetic variance, these two parameters need to be determined for a wide range of plant characteristics. It is essential to measure a wide range of characteristics as it is not known which ones are important for future selection. This also allows the determination of important genotypic correlations. Large negative correlations essentially mean that selection for an increase in one characteristic will lead to a decrease in the other characteristic. This can have important implications when the breeder is selecting for an increase in both characteristics. It is also

necessary to determine the importance of genotype-environment interactions for a wide range of plant characteristics. If genotype-environment interactions are present then it is essential that the plants are selected in the environment in which they are to be used. Therefore it is also essential to use a wide range of environments to determine interactions between genotypes and those environments. Environmental effects can be distinguished using an experiment of this design. As little is known about the environmental effects on *T. ambiguum* this aspect is of considerable importance.

A second experiment was conducted to give information on potential herbage production, management requirements, drought response, root and rhizome yields and seed yields in an established stand of *T. ambiguum* c.v. Treeline under good agronomic conditions in the lowlands.

CHAPTER 2

LITERATURE REVIEW

2.1 INTRODUCTION

Trifolium ambiguum M. bieb. is a strongly rhizomatous, low crowned perennial species with a potentially wide range of adaptation, from alpine habitats down to continental rangelands and steppes. It is commonly known in Australia as Caucasian clover (Bryant, 1974) and as Kura, Honey, Pellett or Deer clover in the United States (Kiem 1954, Pellett 1954).

It occurs naturally throughout Caucasian Russia, Crimea, Central and Eastern Moldavia, North-west Iran and Eastern Turkey (Hossain 1961, Zohary 1970, Khoroshailov and Federenko 1973). It has also been found in Rumania (Negrean, 1968) and Iraq (Townsend, 1974).

Trifolium ambiguum has a number of desirable agronomic properties, most of which are related to its massive rhizome and root system. This makes it a useful legume species for revegetation and erosion control.

2.2 TAXONOMY AND GENETIC CHARACTERISTICS

The taxonomic classification of *Trifolium ambiguum* M. Bieb. as stated by Komarov (1945), Hermann (1954), Townsend (1970) and Zohary (1970) is:

Family - Leguminosae

Genus - Trifolium

Subgenus - Trifoliastrum

Section - Amoria (Euamoria)

Species - ambiguum

Bryant (1974) considers that the closest taxonomic relatives of *T. ambiguum* are *T. hybridum, T. repens* and *T. montanum*. However, Chen

and Gibson (1974) report marked cytological differences. Interspecific hybrids of *T. ambiguum* have been produced with both *T. hybridum* (Kiem 1953, Evans 1962) and *T. repens* (Williams and White 1976, 1977) using embryo culture but they were generally infertile.

Hossain (1961) differentiated *T. ambiguum* into two subspecies, *ambiguum* and *majus*, and a high altitude var. *alpinum* is mentioned by several authors (Busch 1940, Tamamsjan and Fedorov 1949, Vacek and Ded 1956), but these classifications are considered unnecessary because of the recognition of a polyploid series within the species. Hely (1957) found that the species consists of diploids, tetraploids and hexaploids with a basic chromosome number of x=8.

The three ploidy levels within the species have distinct though overlapping ranges of altitudinal adaptation. The diploids are best adapted to high altitudes and the hexaploids best adapted to low altitudes (Baysal 1974, Bryant 1974).

Kannenberg and Elliott (1962) suggested that the optimum ploidy level for some habitats may be higher than hexaploid. However, such forms have not yet been found to occur naturally and so far all octoploids induced by use of colchicine appear to be of little agronomic value (Bryant, 1974).

Zorin *et al.* (1976a) reported that one distinct hexaploid population, cultivar "Prairie" was unable to be crossed with eight other hexaploid populations and for this reason it was thought to be an allopolyploid (Register of Australian herbage plant cultivars 1977). However, no evidence could be found in the literature to indicate whether cv. "Prairie" or any other polyploid population exhibits 'normal' disomic inheritance or the more complex tetrasomic inheritance possible in autopolyploids.

Kannenberg and Elliott (1962) concluded that although most morphological, floral and agronomic characters generally changed with ploidy level, the only accurate means of distinguishing among ploidy levels were chromosome counts.

2.3 MORPHOLOGICAL AND RHIZOME CHARACTERISTICS

The morphological characteristics of *T. ambiguum* have been fully described in the botanical reviews of Komarov (1945), Hermann (1953), Hossan (1961), Zohary (1970) and Townsend (1974). However, the root and rhizome system was poorly described in these reviews. Bryant (1974) described *T. ambiguum* as having a deep semi-woody often branching taproot from which many branched rhizomes grow. These eventually give rise to daughter plants both terminally and from nodes.

Morphologically *T. ambiguum* is a very diverse species (Townsend, 1974). This is most likely due to its strong self-incompatibility system, its ability to reproduce vegetatively and the diverse habitats in which it has evolved. Khoroshailov and Federenko (1973) observed that in 51 naturally occuring populations of unknown ploidy levels plant height varied from 6 to 115 cm, leaflet length from 1.4 to 5.0 cm, petiole length from 9 to 40 cm and stem thickness from 1.5 to 5.0 mm. Similarly, Skripchinskii and Voloshenko (1975) found considerable variation in 26 naturally occuring populations of *T. ambiguum*.

Generally, plant height, leaf size, petiole length, rhizome production and overall plant size increase as the ploidy level increases (Hely 1957, Kannenberg and Elliott 1962, Baysal 1974, Meares 1975). However, there is still considerable morphological variation within each ploidy level, both among and within populations (Kannenberg and Elliott, 1962).

The growth habit of individual spaced plants is not related to ploidy level and most populations contain both prostrate and erect plants (Kannenberg and Elliott 1962, Baysal 1974).

The "root"-shoot ratio of *T. ambiguum*, or the proportion of the plant below ground, was found by Paljor (1973), Meares (1975) and Spencer *et al.* (1975) to be higher than in *T. repens* c.v. "Grasslands Huia". Although their respective results show differences which may be attributable to diverse experimental conditions it is possible to draw some general conclusions from their work. It is clear that the proportion of *T. ambiguum* below the ground increases as the plant matures and produces rhizomes while the proportion of *T. repens* below the ground decreases as the plants produce stolons. At three weeks of age 30 - 35 percent of the dry matter of seedlings of *T. ambiguum* was below ground while "Huia" had slightly less at 25 to 30 percent (Paljor, 1973). After three months, at about the time *T. ambiguum* initiated rhizome production, the proportion of the plant below ground had increased to 50 - 60 percent in *T. ambiguum* and decreased to 20 - 25 percent in "Huia" (Meares, 1975). In 17 month old mature plants, by which time *T. ambiguum* had produced a mass of rhizomes, the below ground proportion had increased to 70 - 80 percent while in "Huia" it had further decreased to 10 - 15 percent (Spencer *et al.* 1975). Harsh edaphic or climatic effects increased the below ground proportions by 5 - 10 percent while Meares (1975) found variety differences within *T. ambiguum* of up to 20 percent.

Because of its massive rhizome system, and the ability to persist and spread under sub-alpine and alpine conditions (Donskova, 1968) *T. ambiguum* has the potential to be a very useful legume for high country revegetation (Costin and Wimbush 1963, Bryant 1971, Prilipko *et al.* 1972, Nordmeyer pers. comm.).

Plate 1. Established *Trifolium ambiguum* plants

Plants of c.v. Prairie established in a high country tussock grassland. Indicator strips are 1 m long.

2.4 FLOWERING AND SEED PRODUCTION

Profuse flowering of *T. ambiguum* generally occurs in late spring and early summer although there is considerable variation in the date of floral initiation (Kannenberg and Elliott 1962, Townsend 1970, Baysal 1974). Despite variation both within and among populations there is a tendency for flowering to be later as the ploidy level is increased (Hely 1957, Kannenberg and Elliott 1962, Baysal 1974).

Townsend (1970) observed a high correlation ($r = 0.85$) for date of flowering of individual plants in two subsequent years. This is an indication that flowering is regulated by a seasonal factor. The observation by Hely (1957) that some populations from the Caucasus region (40 - 45°N) exhibited erratic flowering behaviour when grown at Canberra (34°S), Australia suggests that some plants require long days to initiate flowering. A photoperiodic requirement for c.v. "Prairie" was borne out when it was found that a few hours of artificial lighting each evening caused more regular flowering behaviour (Nordmeyer pers. comm.).

Because of the extremely low self compatibility within all ploidy levels cross pollination is essential to obtain seed yields of *T. ambiguum* (Kannenberg and Elliott 1962, Hely 1963, Townsend 1970, Baysal 1974). However, as bees are readily attracted to its flowers, and the rich nectar they contain (Wykes, 1952), cross pollination is unlikely to be a problem if bees are present (Pellett 1945, 1946, 1948). Bryant (1974) demonstrated that 10 - 12 hives per hectare was optimum for c.v. "Summit" during the dense spring flowering period.

A seed yield of 95 kg ha^{-1} was obtained in c.v. "Summit" despite losing over 50 percent due to heavy rain (Bryant, 1974) while c.v. "Prairie" produced a seed yield in excess of 200 kg ha^{-1} in what was considered a

marginal environment for seed production (Register of Australian herbage plant cultivars 1977). This indicates that the potential seed yield is likely to be greater than 200 kg ha^{-1}.

Despite potentially high seed yields Pellett (1945) found that losses due to pod shattering were a problem. Khoroshailov and Federenko (1973) reported shattering losses to be as high as 50 percent.

Kannenberg and Elliott (1962) have shown that seed set of crosses between ploidy levels of *T. ambiguum* was low. In another species of *Trifolium*, Hagberg (1957) found that a contamination of as little as four percent diploid *T. pratense* reduced the seed yield of tetraploid *T. pratense* by 50 percent. Therefore, as *T. ambiguum* is probably similar, it would be essential to avoid contamination of ploidy levels to maximise seed yields.

2.5 GERMINATION AND SEEDLING ESTABLISHMENT

There is usually a significant proportion of hard seeds in *T. ambiguum* (Bryant, 1974). In 35 naturally occurring populations of unknown ploidy levels Khoroshailov and Federenko (1973) found the mean hard seed content of the viable seed was 89 percent (SD = 9 percent). However, the cultivars developed in Australia are reported to have only 15 - 60 percent hard seed (Barnard, 1972, Register of Australian herbage plant cultivars 1977). Mechanical scarification usually increases the laboratory germination to over 90 percent (Aveyard 1970, Khoroshailov and Federenko 1973).

Bryant (1974) found that the optimum temperature for germination in c.v. "Summit" was 15°C and at this temperature 90 percent of seeds germinated. At both 4°C and 28°C germination remained low at 10 percent. He also found that pre-germination cold-treatment (time period not stated)

at -5°C delayed germination by several days. He considered that this might be a protective mechanism to protect the seed from germination following a false break of spring.

Both seed size and initial seedling vigour are increased with ploidy level and it is likely that differences in seed size account for some of the variation in initial seedling vigour (Kannenberg and Elliott 1962, Paljor 1973, Bryant 1974). Meares (1975) found that the large seeded cultivars of *T. ambiguum* had an initial advantage which lasted for 3 to 4 weeks, from then on the rate of establishment for each cultivar was proportional to its final vigour. Similarly, *T. ambiguum* had an initial advantage over the smaller seeded *T. repens* "Huia" which lasted for 3-4 weeks. After this, the rate of establishment of *T. ambiguum* was poor in comparison to *T. repens*.

In extremely infertile soils, Hely (1963) found that seedling establishment and nodulation was enhanced by applying nitrogenous fertilizer. The nitrogen increased the proportion of late nodulating plants that survived, and subsequently fixed nitrogen by preventing the onset of symptoms of early nitrogen deficiency. Hely (1972) has since stressed the importance of prompt nodulation for plant survival in the low fertility soils often encountered in high altitude revegetation.

2.6 NODULATION

Initially, the inability of *T. ambiguum* to form effective nodules was the major problem in its domestication (Parker and Allen 1952, Hely *et al.* 1953, Kiem, 1954). However, effective *Rhizobium* strains were eventually isolated from soil samples and from nodules on two geographically related species, *T. spadiceum* and *T. ochrolencan*, found in eastern Turkey (Erdman and Means, 1956).

Hely (1957) found that the few strains of rhizobia effective on *T. ambiguum* were totally ineffective on all other common clover species. Consequently, Vincent (1974), in a review of *Rhizobium* strains, lists *T. ambiguum* as the sole member of *Trifolium* host subgroup C.

Hely (1957, 1963) observed that not all *T. ambiguum* plants were nodulated by the available *Rhizobium* strains. He also found a strong positive correlation between earliness of nodule formation and the effectiveness of nitrogen fixation. Because of their superior nitrogen fixation early nodulating plants were found by Hely and Zorin (1975) to have an advantage which persisted for several years over late nodulating plants. By selecting for early nodulation during four generations in the alpine diploid population C.P.I.* 2264, Hely (1971, 1972) tripled the proportion of plants which were nodulated within two weeks of inoculation under laboratory conditions. The cultivar "Summit" resulted from this selection programme (Barnard 1972).

Rhizobium strains found to be effective on one line of *T. ambiguum* were generally found to nodulate most other lines with varying degrees of effectivness (Hely and Zorin 1975, Zorin and Hely 1975, Zorin *et al.* 1976a, Zorin *et al.* 1976b). The most effective Rhizobium strains for lines within each ploidy level, as recommended by Brockwell (pers. comm.) are: diploids CC+231a, tetraploids CC286a and hexaploids CC283b.

Under field conditions there is still a significant proportion of ineffectively nodulated plants despite using the best available *Rhizobium* strains, this is especially true in diploid populations (Hely and Zorin 1975). It is therefore essential for revegetation and agronomic uses that both

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* C.P.I. = Commonwealth Plant Introduction number

\+ CC = Canberra Culture number

Rhizobium strains and *T. ambiguum* populations capable of forming a more efficient symbiosis are selected.

2.7 PHOTOSYNTHESIS AND RESPIRATION

There has been little work done on the rate of photosynthesis and respiration in *T. ambiguum*. The only reported measurements of photosynthesis and respiration rates were done by Paljor (1973). He calculated from his data that *T. ambiguum* had a much lower net assimilation rate and relative growth rate than *T. repens* c.v. "Grasslands Huia". The lower rates he observed in *T. ambiguum* compared with "Huia" were attributed to higher dark respiration rates while the light respiration rates and photosynthetic rates were similar.

Meares (1975) concluded from Paljor's work that *T. ambiguum* has an inherently low production potential even under optimal conditions. This was borne out in observations by both Paljor (1973) and Meares (1975) who found that the growth rate of *T. ambiguum* was inferior to both *T. repens* "Grasslands Huia" and *Lotus pedunculatus* "Grasslands Maku" when grown in pots under glasshouse conditions.

2.8 RESPONSE TO ENVIRONMENTAL FACTORS

2.81 TEMPERATURE

Paljor (1973) and Meares (1975) found that *T. ambiguum* plants grown at day temperatures of 10°C in growth cabinets were smaller in every respect than plants grown at 20°C. At the lower temperature there was also poorer nodulation and an increase of 10 to 15 percent in the proportion of the plant below ground. As expected, plants from the alpine diploid population, c.v. "Summit" performed relatively better at low temperatures (Paljor 1973, Meares 1975).

Bryant (1974) observed that in alpine regions of the Snowy Mountains, Australia, a diploid population (C.P.I.2264) had superior persistence to a tetraploid population (C.P.I.6884). Hexaploid populations were least persistent and were most affected by frosts during the growing season. However the hexaploids were equivalent in persistence to *T. repens*, *T. hybridum* and *T. fragiferum*.

Under natural conditions in the alpine regions of the Caucasus Mountains Donskova (1968) found that individual plants of *T. ambiguum* (most probably diploid) persisted for up to 18 years. Although plants survived for a long time it should be noted that under the harsh alpine conditions the whole of their life cycle was slowed down.

Meares (1975) found that *T. ambiguum* exhibited marked winter dormancy compared to *T. repens* "Grasslands Huia" when grown under lowland New Zealand conditions. Under lowland conditions winter dormancy is not essential for survival and winter active cultivars would need to be selected before *T. ambiguum* could be used efficiently in the lowlands. However, in alpine regions winter dormancy may be essential for plant survival.

2.82 LIGHT

No evaluation has been made of the effects of light intensity and daylength on *T. ambiguum*. However, indications are that daylength is likely to influence flowering behaviour (Hely 1957, Townsend 1970, Meares 1975) while light intensity would be expected to influence photosynthesis and consequently, herbage production. Meares (1975) considers that, like other clover species, *T. ambiguum* is likely to be intolerant of shading. This is supported by the work of Khoroshailov and Federenko (1973) who reported that plants were generally found in sunny areas.

2.83 SOIL MOISTURE

Khoroshailov and Federenko (1973) observed that *T. ambiguum* is

responsive to soil moisture but does not grow in permanently waterlogged areas. However, Bryant (1974) found that some lines had high survival rates after periods of flooding for up to 40 days in the early spring. In addition, some diploid lines are very drought tolerant (Zorin *et al.* 1976c). Attempts are therefore being made in Australia to select drought tolerant forms from all ploidy levels (Bryant 1974).

2.84 EDAPHIC FACTORS

Bryant (1974) considers that *T. ambiguum* has a general preference for non-calcareous soils. However, Khoroshailov and Federenko (1973) reported growth of naturally occuring populations of *T. ambiguum* on limestone soils, saline soils and the black soils of mountain meadows in the U.S.S.R. Baysal (1974) reports that his collection sites in Turkey were on volcanic soils of pH 7.4 to 8.4.

Agababyan (1960) found that *T. ambiguum* was able to grow at low pH (4.9) under sub-alpine conditions in the Armenian S.S.R. where *T. repens* and other introduced species failed to persist. Although *T. ambiguum* can persist in acidic soils it is likely that nodulation would be restricted under these conditions. In pot trials, Paljor (1973) found that in c.v. "Summit" nodulation was restricted at low pH, at least below 5.1.

Barnard (1972) recommended c.v. Summit as a cultivar suitable for planting under low phosphate conditions where it was found to grow and persist better than *T. repens*. Its ability to grow under low phosphate conditions is probably largely due to its massive root and rhizome system enabling a greater volume of soil to be explored. The ability of *T. ambiguum* to grow at low phosphate levels does not mean that it can not respond to high levels of phosphate. Both Paljor (1973) and Meares (1975) found that *T. ambiguum* was

highly responsive to phosphate additions. Similarly, under field conditions it has been found to compete better with grasses when phosphate was applied (Agababyan 1966, Zotov 1967, Teberdiev 1970).

2.9 PRODUCTIVITY AND MANAGEMENT

There have been few field measurements of herbage production of *T. ambiguum*, the only reported measurements were carried out in Australia and U.S.S.R. At an altitude of 370 m in the North Caucasus, Lubenets (1968) compared the production of $5m^2$ pure swards of *T. ambiguum* with local varieties of *T. pratense*. The plots were sown in 1958 and the herbage yields were measured in 1959, 1961 and 1963. *T. ambiguum* yielded 200, 1060 and 900 gm^{-2} fresh weight while *T. pratense* produced 740, 2400 and 300 gm^{-2} fresh weight for the three years respectively. At 18 to 22 percent dry matter content* the *T. ambiguum* herbage yields would be equivalent to 320-400, 1700-2100, 1450-1800 kg ha^{-1} dry matter while the *T. pratense* yields would be equivalent to 1200-1480, 3800-4800, 480-600 kg ha^{-1} for the three years respectively. The higher yield of *T. ambiguum* in the fifth year, compared to *T. pratense*, is most likely a reflection of its superior persistence. However, as *T. ambiguum* produced less in the first year the rate of establishment may be slower. Higher yields of *T. ambiguum* were obtained by Kasirina (1956) near Leningrad. She measured the herbage yield of a first year stand of *T. ambiguum* as 28,000 kg ha^{-1} fresh weight (probably equivalent to 4600-5400 kg ha^{-1}). This was obtained from two cuts, the first yielded 20,000 kg ha^{-1} fresh weight while the second, 17 days later, yielded 8,000 kg ha^{-1} fresh weight. Yields in the second year were reported to be less than the first year because of poor weather conditions. Similarly, Busch and Schmidt (1938) found that *T. ambiguum* grew well in its first season, but they did not state the yield.

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* typical dry matter percentages for *T. ambiguum* obtained in Experiment two

None of the Russian authors describe the *T. ambiguum* populations used but it is likely that they were unselected, at least for efficient nodulation. As Hely (1957) has shown that in general unselected populations of *T. ambiguum* have inefficient nodulation the relatively low yields obtained by these researchers may have been due in part to poor nodulation. It should also be noted that because of the large proportion of *T. ambiguum* below the ground, up to 76 percent (Spencer *et al.* 1975), the total plant dry weight of *T. ambiguum* may not have been much less than the *T. pratense*.

In Australia, at altitudes of 650 m and 1310 m in Victoria, Spencer *et al.* (1975) compared two cultivars of *T. repens*, "Tasmanian Bothwell" and "Grasslands Huia", with two lines of *T. ambiguum*, c.v. "Summit" and C.P.I. 50329 (6x). All the plants were established in pots and transplanted to the field. After 17 months the total plant yields, including roots and rhizomes, of the two white clover cultivars and C.P.I. 50329 at the two sites ranged from 6650 to 6980 kg ha^{-1}. The *T. ambiguum* line C.P.I. 50329 had 76 percent of its dry matter below ground while in white clover only 13 to 15 percent of the total dry matter was below the ground. The mean total plant dry weight of cultivar "Summit" at the two sites was 5510 kg ha^{-1}, 70 percent of which was below the ground.

As to its properties as a stock feed, *T. ambiguum* is reported in the Register of Australian herbage plant cultivars (1977) to be non-oestrogenic. It is also highly palatable (Pellet 1948, Bryant 1974) with a protein content reported by Agababyan (1934) and Kasirina (1956) as 16 percent of the dry matter. However, the herbage has a low tannin content (Currier pers. comm.) and if it was the major proportion of a ruminant's diet it might cause bloat.

Vacek and Ded (1957) consider that *T. ambiguum* is a hay type species. In this respect Agababyan (1934) reports that it is capable of giving three

cuts per season while Zivov and Skvorcov (1951) refer to a two cut variety. As well as being a hay type species Petrosyan (1970) found that it could be used to produce high quality silage.

Burova (1955) reported that in areas of natural occurance *T. ambiguum* is held in high regard for its high quality early season growth. On the other hand, Agababyan (1960) and Donskova (1969) valued *T. ambiguum* for its persistance under heavy grazing despite Abromova's (1951) observation that it died out in the second year. In spite of the observation by Khoroshailov and Federenko (1973) that *T. ambiguum* did not grow in permanently waterlogged areas it has been recommended by Rokzov (1949), Malygin (1953) and Nenarokov (1956) as being suitable for 4-7 year leys in wet low relief soils where *T. pratense* failed to grow. Similarly, Kiem (1954) suggested that it would be suitable for soils which were too wet for lucerne.

2.10 DISEASE AND PEST RESISTANCE

Nordmeyer (pers. comm.) observed that *T. ambiguum* has persisted in an area which was heavily infested with grass grub (*Costelytra zealandica*) where both *T. repens* and *T. hybridum* were killed. However on examination it was found that the plants had not escaped completely unharmed as the roots and rhizomes had been partially eaten by the grassgrub.

Trifolium ambiguum was reported by Norton and Isely (1967) to be a host for the Clover Cyst Nematode (*Heterodera trifolli*), but it appeared to be much more resistant to it than *T. repens*.

Barnett and Gibson 1975 found that *T. ambiguum* was also resistant to seven common virus diseases which affect *T. repens* in the United States of America.

Meares (1975) found that *T. ambiguum*, especially the parent line of

c.v. "Prairie", C.P.I. 10803, was very susceptable to downy mildew under glasshouse conditions. Similarly, Khoroshailov and Federenko (1973) found that some populations were susceptable to powdery mildew in the field but as differences between populations were observed it should be possible to breed cultivars resistant to these diseases.

2.11 SELECTION AND BREEDING

Several breeding programmes involving *T. ambiguum* have been carried out in various parts of the world. The only reported selection within the U.S.S.R. was that of erect forms by Kupcov (1935). However, as Zivov and Skvorcov (1951) refer to the "early 2 cut variety 820" is likely that this was also a selection.

In the U.S.A., Townsend (1975) has registered a hexaploid line of *T. ambiguum* designated "C-2 Kura clover". This selection was the seed from 20 well nodulated vigorous plants of diverse origin grown at Fort Collins, Colorado.

There are four cultivars of *T. ambiguum* registered in Australia, cvv. "Summit" (2x), "Forest" (2x), "Treeline" (4x) and "Prairie" (6x). The origin, morphology and agronomic characteristics were described by Barnard (1972) and the register of Australian herbage plant cultivars (1977).

The four Australian cultivars were selected for early nodulation, seedling vigour, flowering ability, seed set and survival under field conditions.

Hely (1975) suggested that discretion is needed in breeding for increased nodulation and seed production because both rhizomatous habit and persistence were markedly decreased. Hely and Zorin (1975) found that in dense sowings of c.v. "Summit", which formed closed stands, the earlier nodulating plants acted

as nurse plants for the less well nodulated plants. However, the less well nodulated plants were more rhizomatous and they ultimately spread out to form most of the stable stand. As only the well nodulated less rhizomatous plants flowered in the first year there would obviously be a bias towards lower rhizome production from seed collected in the first year of a stand. This would have obvious implications for seed production in this cultivar and probably the species in general.

2.12 SUMMARY

Trifolium ambiguum is a genetically and morphologically diverse species adapted to a wide range of environmental conditions. It is particularly noted for its ability to grow and persist under both harsh climatic and edaphic conditions where domesticated legume species often lack persistence.

Most of the unique features of *T. ambiguum* are related to its massive root and rhizome system, a feature which makes it a useful legume for revegetation and erosion control. It also has a number of desirable properties for use as a forage legume in pastures. These include: winter and drought hardness on one hand yet tolerance to short periods of flooding on the other, resistance to some serious clover pests and diseases, ability to grow in acidic and low phosphate soils, and palatability and apparent persistence once established. However, it has a very slow initial growth rate and a low herbage production in comparison to the domesticated legumes such as *T. repens*.

For both revegetation and agronomic uses *T. ambiguum* needs efficient nitrogen fixation. At present nodulation and nitrogen fixation are poor in comparison to other domesticated forage and pasture legumes, but with continued selection to improve this the full potential of *T. ambiguum* may be realised.

CHAPTER 3

EXPERIMENTAL MATERIALS AND METHODS

3.1 EXPERIMENTAL PROCEDURES; EXPERIMENT ONE

Introduction

The experiment was designed to investigate the environmental responses and genetic variation of *T. ambiguum* compared with *T. repens* and *Lotus pedunculatus*. The experiment was a 191 x 5 factorial of genotypes and environments with two replicates of each genotype. The 191 genotypes consisted of 180 *T. ambiguum*, 5 *T. repens* and 6 *L. pedunculatus*.

Genetic material

Two lines from each of the three ploidy levels found in *T. ambiguum* were chosen to ensure a wide range of genetic material. To represent variation within each line 30 genotypes were selected for use. Within the six lines four are registered Australian cultivars and two are Commonwealth Plant Introductions (Commonwealth Plant Introduction Review 1970, 1972, Barnard 1972, Register of Australian herbage plant cultivars 1977). The lines were c.v. "Summit" (2x), c.v. "Forest" (2x), C.P.I. 51140 (4x), c.v. "Treeline" (4x), C.P.I. 57353 (6x) and c.v. "Prairie" (6x). The ploidy levels were confirmed by cytological examinations of one 'typical' genotype from each line.

For comparison five genotypes of *T. repens* "Grasslands Huia" and six genotypes of *Lotus pedunculatus* "Grasslands Maku" were included.

Environments

To ensure a wide range of environmental conditions the environments chosen for the experiment were a 2 x 2 + 1 factorial of altitudes and soils.

This allowed climatic and edaphic effects to be distinguished.

To implement the design $6m^3$ of the top 30 cm of a Wakanui silt loam was transported to Craigieburn and deposited to a depth of 20 - 25 cm on an area where the natural topsoil had been removed. Similarly $6m^3$ of Cass soil, $3m^3$ of topsoil and $3m^3$ subsoil were transported to Lincoln College where they were deposited to a depth of 20 - 25 cm, 10 cm subsoil and 10 - 15 topsoil, on to an area where the natural topsoil had been removed. In both cases the surface was flush with the surrounding area and was expected to maintain normal water relationships.

The environments used were as follows:

altitude a.s.l. site	Soil	Referred to as
12 m Lincoln College	Wakanui Silt Loam	Wak/low
12 m Lincoln College	Cass *	Cass/low
800 m Cave Stream, Craigieburn	Wakanui Silt Loam*	Wak/med
800 m Cave Stream, Craigieburn	Cass	Cass/med
1200 m Mt. Cochane, Craigieburn	Bealey	Bealey/high

* Soil transplants

The soils were identified from descriptions given in the New Zealand Soil Bureau Bulletin, number 26 (1968).

Fertilizer was applied to the Cass and Bealey soils at rates equivalent to 50 kg ha^{-1} P, 100 kg ha^{-1} K, 100 kg ha^{-1} Mg, 80 kg ha^{-1} S, 100 g ha^{-1} Mo. These were applied as Superphosphate, K_2SO_4, $MgSO_4.7H_2O$, Na_2MoO_4 and were expected to correct the soil deficiencies known to exist. Fertilizer was not applied to the Wakanui soil as no deficiencies were

expected. The soil analysis values and climatic data for each site are presented in Appendix A.

Preparation of Plant Material

Rhizome cuttings of *T. ambiguum* were taken in June 1977 from spaced plants at Lincoln College and were established in sterile potting mix in 10 cm long 20 mm diameter alkathene tublings. Stolon and stem cuttings of Huia and Maku respectively were also established in similar tublings.

To ensure that all plants were adequately nodulated with effective strains of rhizobia all *T. ambiguum* plants were inoculated in July by injecting each tubling with 1 ml of *Rhizobium* solution. The solution was a mixture of the three strains of rhizobia recommended by Brockwell (pers. comm.), CC231a for diploids, CC286a for tetraploids and CC283b for hexaploids. The solution contained more than 10^6 rhizobia ml^{-1} (Close pers. comm.).

For Huia and Maku the appropriate commercial strains were applied by watering the solutions over the tubling plants.

The plants were grown in a glasshouse until September when they were transfered to a shade house where they remained until planting out. During the time they were in the glasshouse c.v. "Summit" became infected with *Fusarium* and *Rhizoctonia* (McCully pers. comm.). Some plants died before the disease was controlled by the application of "Benlate" at the recommended rates. However, as there were an excess number of plants established the surviving plants were healthy and the disease did not affect the experiment in any way.

Transplanting

All experimental sites except the high altitude one were rotary hoed prior to transplanting. The high altitude environment was cleared of

vegetation by grubbing and then immediately transplanted. All experimental sites were watered prior to transplanting with a mixture containing the three *T. ambiguum* strains of rhizobia. This was in addition to the tubling inoculation.

The planting pattern consisted of 18 rows of *T. ambiguum* with 20 plants per row and a single row each of Huia and Maku. All the *T. ambiguum* plants were completely randomised within the 18 rows and were spaced 30 cm apart both within and between rows.

The tublings were transplanted into the trial sites on the following dates:

Wak/low	17 October
Cass/low	16 November
Wak/med	27 November
Cass/med	30 November
Bealey/high	25 November

Visual scores were taken for both top and root growth at transplanting. These were intended for use in covariance adjustment on final yields. However, as the covariance adjustment accounted for an insignificant amount of the variation it was not used.

Plants at all the experimental sites were watered twice weekly for three weeks after transplanting to aid establishment and this was continued for the whole season on both soils planted at the Lincoln College site.

General Measurements

Plant morphological characteristics were measured in February 1978 and plant dry weights were obtained at harvest in March 1978. Harvesting involved counting numbers of both flowers and daughter plants, removing the

top growth and determining the oven dry weights of the top growth. The remaining basal portion of the plants were then removed from the soil and washed, disected into roots and rhizomes, measured, oven dried and weighed. Flowers at both Lincoln College sites were removed and weighed separately to determine flower dry weight per plant but at the other sites the flowers were harvested with the other top growth.

Leaf area per largest leaf was measured at both Lincoln College sites but could not be measured for all sites. This was because of the difficulties involved in collecting, transporting and keeping the samples fresh enough to be measured with the area meter.

A detailed study of rhizome growth characteristics was undertaken of plants from the medium elevation sites to determine the effect of contrasting soils on rhizome growth.

Description of Measurements on Individual Plants

ROOT VIGOUR: At transplanting the number of centimetres of root protruding out the bottom of each tubling was visually assessed. Rhizome growth was ignored for this assessment.

SHOOT VIGOUR: At transplanting the number of leaves were counted.

LEAF MARKINGS: All the genotypes used in the experiment were recorded for the presence of pale V or U shaped markings on the leaves.

MULTIPLE LEAFLETS: All the genotypes used in the experiment plus 20 more of each variety were recorded for the presence of more than three leaflets.

LEAF AREA: The trifoliate leaf which appeared to have the largest area was chosen by visual assessment from each plant, the petiole was removed and the area measured using a Licor model 3100 area meter. Only plants

growing at the two Lincoln College sites were measured for this parameter.

LEAFLET LENGTH: The length of the middle leaflet on the largest leaf chosen by visual assessment (same leaf as above) was measured for all plants at all sites.

LEAFLET WIDTH: The width of the middle leaflet on the largest leaf chosen by visual assessment (same leaf as above) was measured for all plants at all sites.

LEAFLET LENGTH-WIDTH RATIO: The ratio of the two previous measurements was calculated.

PETIOLE LENGTH: The length of the petiole supporting the largest leaf as chosen for leaflet length and width was measured for all plants at all sites.

PLANT HEIGHT: The maximum height of leaves vertically above ground as they occurred naturally was measured for all plants at all sites. Although flowers often extended above the canopy these were not included in this measurement.

PLANT WIDTH: The maximum width of the parent plant's vegetative growth was measured as it occurred naturally. This measurement did not include flowers or new plants arising from rhizomes and was carried out on all plants at all sites.

PLANT HEIGHT-WIDTH RATIO: The ratio of the two previous measurements was calculated to give an indication of the growth habit of the parent plant. A high value for this measurement indicated an erect plant while a low value indicated a prostrate plant.

VEGETATIVE TOP DRY WEIGHT: The oven dry weight of leaves and petioles was measured for the two Lincoln College sites. Flowers were excluded from

this measurement. This measurement contains practically all the vegetative growth produced over the growing season as very few leaves died and got lost.

TOP DRY WEIGHT: The oven dry weights of all the above ground plant material was included in this measurement, that is, flowers, leaves and petioles. For the two Lincoln College sites it was obtained by adding flower dry weight to vegetative top dry weight.

PROPORTION TOP DRY WEIGHT: This was calculated by dividing top dry weight by total plant dry weight.

NUMBER OF FLOWERS: The number of flowerheads was counted at harvest for all plants at all sites. In some plants which flowered early mature flowerheads were collected in December and stored. The number of flowerheads collected in December was added to the number counted at harvest to obtain the number of flowers produced for the season.

FLOWER DRY WEIGHT: The air dry weight of flowers was corrected to oven dry weight, by multiplying by the dry matter proportion of samples, to determine flower dry weight. This measurement was only carried out for the two Lincoln College sites.

DATE OF FLOWERING: All plants at all sites were recorded every 7 to 10 days over the season to determine presence or absence of flowerheads. The first date at which a flowerhead was mature enough to be pollinated by a bee was taken to be the date of flowering.

PROPORTION FLOWER DRY WEIGHT: This was calculated by dividing flower dry weight by total plant dry weight.

ROOT DRY WEIGHT: Plants at all sites were dug from the soil, using a fork, to a depth of 25 cm only. The plants were washed, the rhizomes were removed as were any remaining leaves, and the remaining root and crown was

oven dried and weighed to obtain root dry weight. Some roots were left in the soil but none of these were greater than 3 mm in diameter.

PROPORTION ROOT DRY WEIGHT: This was calculated for plants at all sites by dividing root dry weight by total plant dry weight.

LENGTH OF LONGEST RHIZOME: The length of the longest primary rhizome was measured on each plant at all sites.

NUMBER OF NODES: The number of nodes found on the longest rhizome was counted at the two medium elevation sites.

INTERNODE LENGTH: The length of the longest rhizome was divided by the number of internodal segments to obtain the mean internode length. The number of internodal segments equals the number of nodes plus one. The measurement was therefore the mean internode length and no attempt was made to determine the variation in length along the rhizome. This measurement was only calculated for the medium elevation sites.

PROPORTION OF NODES BRANCHING: For the two medium elevation sites the number of branches forming at nodes on the longest rhizome was divided by the total number of nodes to give a measure of apical dominance. A record of whether the rhizome had emerged to form a daughter plant was kept as this was thought to influence apical dominance.

NUMBER OF RHIZOMES: The number of rhizomes coming from the plant crown were counted on plants at all sites.

NUMBER OF DAUGHTER PLANTS: The number of daughter plants which appeared to belong to the parent plant was counted for plants at all sites. It was not, however, always possible to identify to which parent plant the daughter plant belonged.

RHIZOME DRY WEIGHT: The oven dry weight of washed rhizomes, separated from roots, was determined for plants at all sites.

PROPORTION RHIZOME DRY WEIGHT: This was calculated for plants at all sites by dividing rhizome dry weight by total plant dry weight.

TOTAL PLANT DRY WEIGHT: This is the sum of root dry weight, rhizome dry weight and top dry weight and was calculated for plants at all sites.

3.2 STATISTICAL MATERIALS AND METHODS

Introduction

The analysis was performed using 29 Forest genotypes, 22 Summit, 30 C.P.I. 51140, 27 Treeline, 28 C.P.I. 57353 and 29 Prairie genotypes. The remaining 15 genotypes were discarded because no replicates at a given site had survived, or because of "off-types" within the genotype. The total number of plants of each variety at a given site which were used for analysis are listed in Appendix B.

Analysis of Variance

The computer program GXE (Appendix C) was written and used to perform analysis of variance on the 165 *T. ambiguum* genotypes.

To correct for heterogeneity of variance among environments all the data from each environment was weighted by the reciprocal of the standard deviation of genotype means as performed by Johnson (1977).

As recommended by Finney (1973) counts up to 20 or 30 were transformed by square root while percentages outside the range of 30 to 70 were transformed by arcsine. No other transformations were performed.

The environment mean square was further partitioned to determine soil and climatic effects. The climatic effect was determined by comparing the

mean of the two soils at low altitude with the mean of the two soils at medium altitude. Similarly, the soil effect was determined by comparing the mean performance on the Wakanui soil at both locations with the mean of the Cass soil. The genotype-environment interaction mean square was also partitioned into soil and climatic effects in the same way. This analysis was performed using the "Teddybear" statistical package (Wilson 1976).

Comparison of Variety Means

The variety means presented in the results were the means of all genotypes within a variety. No backtransformed means were presented.

To test variety means within each environment Scheffé's least significant difference was used. This method of comparison allowed for the unequal number of genotypes and was a very conservative test (Chew 1976). Scheffé's least significant difference was determined by pooling the variance of genotype means for all varieties, including c.v. Huia and c.v. Maku where appropriate.

Genotypic Coefficients of Variation

The genotypic coefficients of variation were calculated as follows (Burton 1952):

$$GCV\% = \frac{SD_G}{\bar{X}} \times 100$$

where SD_G = standard deviation of genotype means

$\bar{X}$ = mean

Heritability Estimate

The bread sense heritability was determined by separating the mean squares from the analysis of variance table into components of genotypic

variance, genotype-environment interaction variance and within environment variance. These were determined in the following way (Breese 1969).

Table 1: Partition of mean squares from the analysis of variance into genotypic coefficients of variance.

Source	df	Expected Mean Square
Genotype	g-1	$\sigma^2 + r\sigma^2_{GE} + re\sigma^2_G$
Environment	e-1	$\sigma^2 + r\sigma^2_{GE} + rg\sigma^2_E$
GXE	(g-1)(e-1)	$\sigma^2 + r\sigma_{GE}$
Error	difference	σ^2

where σ^2 = within environment variance

r = number of replicates

e = number of environments

g = number of genotypes

σ^2_{GE} = interaction variance

σ^2_G = genotypic variance

σ^2_E = between environment variance

The heritability was then calculated by dividing the genotypic variance by the phenotypic variance as follows:

$$h^2 = \frac{\sigma^2_G}{\sigma^2_G + \sigma^2_{GE} + \sigma^2}$$

All these calculations were performed using the GXE computer program.

The standard error of the heritability estimate was calculated using extensions of the models developed by Becker (1967) and Gorden (*et al.* 1972, *pers. comm.*).

The standard error of the heritability estimate was calculated by taking the square root of the variance of the heritability estimate. The variance of the heritability estimate as stated by Osborne and Paterson (1952) and Kempthorne (1957) was:

$$V(h^2) = (G^2V(P) + P^2V(G) - 2PG\ Cov(P,G))/\ P^4$$

where G = genotypic variance

P = phenotypic variance

V(G) = variance of the genotypic variance

V(P) = variance of the phenotypic variance

Cov(P,G) = covariance between genotypic and phenotypic variance

The variance of the genotypic variance was estimated as follows (Kempthorne 1957, Gordon *pers. comm.*):

$$V(G) = \frac{2}{k^2} \sum_{n=1}^{n} \left(\frac{MS_n^{\ 2}}{fn + 1} \right)$$

where MS_n = nth mean square in the linear function of mean squares, k is the coefficient associated with G in its mean square (i.e.: number of replicates x the number of environments), and fn = degrees of freedom of nth mean square.

The variance of the phenotypic variance was estimated as follows (Gordon *pers. comm.*):

$$V(P) = V(e) + V(I) + V(G) + 2(Cov(e,I) + cov(e,G) + cov(I,G))$$

where V(e) = variance of error variance and

V(I) = variance of interaction variance

Both V(e) and V(I) are estimated in the same way as V(G) (i.e.: assuming a linear combination of mean squares).

Cov(e,I) was determined from Gordon (*pers. comm.*) to be $-V(e)/n$ where n = the number of replicates and V(e) = variance of error variance.

Cov(I,G) = $-V(I)/E$ where E = number of environments and V(I) = variance of interaction variance.

Cov(e,G) = $(V(e)/n - V(e))/nE$

Lastly, cov(P,G) was calculated in the following way:

= V(G) + cov(e,I) + cov(I,G) + cov(e,G)

The standard error of the heritability was calculated in the program GXE using the above method.

Correlations

The correlations were calculated using the methods described by Scheinberg (1966). The following formula was used for phenotypic and genotypic correlations:

$$r = \frac{V_{12}}{\sqrt{V_{11} \times V_{22}}}$$

where V_{11} and V_{22} were the genotypic or phenotypic variances and V_{12} was the genotypic or phenotypic covariance of the two parameters correlated. The phenotypic variance or covariance was equivalent to the genotype mean square in the analyses of variance and covariance respectively. The genotypic variance or covariance was the component of the genotype mean square as partitioned up in table 1 (page 32).

The computer program GENCOR presented in Appendix C was written exclusively to determine phenotypic and genotypic correlations for the experimental design used.

Factor Analysis

Factor analysis was performed using the genotypic correlations among 25 characteristics. The first four factors, together explaining 76% of the variance, resulting from orthogonal rotation are presented in the results. This analysis was performed using the statistical computer package "BMD" (Dixon 1974).

Linear Regression Technique

The linear regression technique developed by Finlay and Wilkinson (1963) for comprehending genotype-environment interactions was attempted for all the characteristics measured on the 165 *T. ambiguum* genotypes. If the technique was to be of any use it must account for a high proportion of the genotype-environment interaction.

The computer program GXE partitions the genotype-environment interaction effect up into 'heterogeneity of regressions' and deviations or 'residual'. The heterogeneity of regression term will be significant if some of the regression lines for individual genotypes have significantly different slopes. The heterogeneity of regression sums of squares is further partitioned into 'convergence' and 'nonconvergence'. The convergence term is a measure of whether the regression lines converge to a point, if they do then a cultivar selected for highest yield in one environment will be the highest yielding in all others. All the above terms were calculated using the statistical methods described by Eagles *et. al.* (1977). The program GXE also calculates Hanson's (1970) stability parameter for each genotype.

The results showed that although the individual regression were generally significant when the raw data was used, the use of weighted data

had the effect of making the regressions not significant. Therefore the linear regression technique was discarded. The failure of the data to produce significant effects was most likely due to having too few environments with different limiting factors at each. Knight (1970) suggested that these factors have to be satisfied before the technique was valid.

3.3 EXPERIMENTAL PROCEDURES; EXPERIMENT TWO

Introduction

This experiment was designed to measure the herbage production from pure swards of *T. ambiguum* c.v. Treeline given different cutting treatments over one growing season from September 1977 until June 1978.

Materials and Methods

The stand was established as spaced plants, 50 cm apart in rows 100 cm apart, in 1973 at the Forest and Range Experimental Station, Forest Research Institute, Rangiora. By the time this experiment was started the plants had spread out to form a dense sward.

The stand was growing on a Wakanui Silt Loam soil (Soil Bureau Bulletin, Number 26 1968). Meteorological data applicable to the site is presented in Appendix A.

The stand had never been grazed but had been cut for seed production every year. However, all herbage was returned to the site. Weed control was performed every winter by hand rogueing. The site was fertilized with superphosphate at planting in 1973 and had not received fertilizer since.

The experimental design used was a 2 x 3 + 1 factorial of cutting height and frequency. The one extra treatment consisted of uncut plots for

the observation of flowering behaviour. The two heights of cutting were to simulate hard and lax grazing. To simulate short, medium and long rotation intervals, the treatments used were to cut monthly, 2-monthly or at flowering. However, in this last treatment flowering only occurred once, in November, so that the sward in this treatment was only cut the one time.

The experiment was laid out in a randomised block design with seven $1m^2$ plots within each of 18 blocks. Therefore the resulting treatment means presented are for an $18m^2$ area.

Spray irrigation was applied weekly to 9 of the 18 blocks from January to April after it became obvious that there would be very little growth without irrigation. This changed the experiment to a split-plot design involving irrigation, height and frequency of cutting.

The plots were sampled with hand-clippers or by powered hedge-clippers and the samples were weighed immediately to determine fresh weight. A sub-sample of about 500 g from each treatment was oven-dried to determine dry matter percentage and from these dry matter yields of whole plots were calculated.

Visual scores of the number of flowers on a 0-10 scale were taken before the November and December cuts to assess the treatment effects on flowering. Similarly weed ingress was scored before each cut from October onwards.

The seed yield from two 1 m^2 quadrats was determined in January from the uncut unirrigated border area. To minimise seed loss all the above ground plant material was cut and bagged.

To determine below ground dry matter one ½ m^2 sample from the uncut unirrigated border area was dug to a depth of 80 cm on 6 June 1978. The sample obtained was then washed and oven-dried. No attempt was made to separate roots and rhizomes.

CHAPTER 4

RESULTS

The results of the two experiments are presented separately and are divided into sections related to each parameter studied.

4.1 EXPERIMENT ONE

Root Vigour at Transplanting

Table 2 (page 40) presents the mean root vigour scores for each variety before transplanting into all the environments. From this table it is clear that Prairie had the lowest mean root vigour score at all sites and Summit lacked 'vigour' in the Wakanui soil at low altitude.

As the root growth of both Maku and Huia was markedly different from *T. ambiguum*, root vigour scores were not assessed for them. In general, root growth of Maku was greater than in the *T. ambiguum* varieties while Huia had less.

Shoot Vigour at Transplanting

The mean shoot vigour scores for each variety before transplanting into each site are presented in Table 3 (page 41). From this table it is apparent that Forest and Summit were generally less vigorous at transplanting than the four polyploid varieties, however, they were not always significantly less vigorous.

As the growth habit and top growth of Maku and Huia were decidely different to those of the *T. ambiguum* varieties their top growth was not scored. However, both Maku and Huia had noticeably more top growth than any of the *T. ambiguum* varieties.

Table 2: Root vigour scores at transplanting, variety means at all environments

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	3.1 ab	4.2 a	4.5 a	4.2 ab	3.6 a
Summit	2x	2.0 b	4.2 a	3.9 a	4.1 ab	3.1 a
51140	4x	4.1 a	4.1 a	3.7 ab	4.5 ab	3.6 a
Treeline	4x	2.9 ab	3.4 ab	4.2 a	4.4 ab	3.7 a
57353	6x	3.9 a	3.8 a	3.7 ab	4.6 a	3.5 a
Prairie	6x	1.9 b	2.1 b	2.4 b	3.0 b	2.4 a
SLSD(5%)		1.47	1.47	1.39	1.51	1.44

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Table 3: Shoot vigour scores at transplanting, variety means at all environments

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	3.5 b	5.2 b	4.2 c	4.2 c	4.0 bc
Summit	2x	2.9 b	6.1 ab	4.5 bc	4.7 c	3.8 c
51140	4x	5.1 a	5.8 b	5.0 bc	5.1 bc	5.2 ab
Treeline	4x	5.2 a	7.1 a	6.9 a	7.3 a	6.4 a
57353	6x	4.8 a	5.8 b	5.7 ab	6.3 ab	5.4 a
Prairie	6x	4.9 a	6.2 ab	5.6 b	6.5 a	5.7 a
SLSD(5%)		1.11	1.18	1.31	1.29	1.36

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Area of Largest Leaf

The variety means for the area of the largest leaf at the two lowland experimental sites are presented in Table 4 (page 43). From this table it is clear that 57353 had the largest mean leaf area while the diploids, Forest and Summit, had the smallest leaf area of any *T. ambiguum* variety. Prairie, Treeline and 51140 were intermediate between 57353 and the diploids.

Although there was considerable overlap among ploidy levels there appeared to be a tendency for leaf area to increase with ploidy level.

Maku and Huia had smaller leaf areas than all the *T. ambiguum* varieties but they were not always significantly smaller than the diploid *T. ambiguum* varieties.

In general, the Cass soil produced plants with smaller leaves than did the Wakanui soil but part of this difference may be due to later transplanting into the Cass soil.

Middle Leaflet Length

The variety means for middle leaflet length of the largest leaf on each plant at all experimental sites are presented in Table 5 (page 44). From this table it is obvious that both Forest and Summit had shorter leaflets than the four polyploid varieties of *T. ambiguum*. This distinction is very clear at all sites except in the Wakanui soil at medium elevation where Prairie and Forest were not significantly different.

Both Maku and Huia had shorter leaves than all the *T. ambiguum* varieties, however, at two of the sites Huia was not significantly different from the diploids.

Table 4: Variety means for leaf area (cm^2) of the largest leaf at the two Lincoln College sites

Variety	Ploidy	Wakanui Soil	Cass Soil
Forest	2x	10.2 c	9.6 cd
Summit	2x	8.9 cd	9.7 cd
51140	4x	11.9 bc	11.1 bc
Treeline	4x	13.8 b	13.6 ab
57353	6x	18.1 a	15.6 a
Prairie	6x	13.9 b	11.4 bc
Maku		5.7 de	4.3 e
Huia		4.6 e	7.6 d
SLSD(5%)		3.45	3.24

Variety means within either environment with the same letter beside are not significantly different using Scheffe's least significant difference at 0.95, probability (SLSD(5%)).

Table 5: Variety means for middle leaflet length of the largest leaf at all environments (millimetres)

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	28.1 c	25.9 cd	28.4 cd	20.9 c	19.3 b
Summit	2x	26.5 c	26.6 c	25.9 d	19.9 c	19.7 b
51140	4x	42.1 a	39.9 a	39.2 a	30.4 ab	29.1 a
Treeline	4x	36.8 b	35.6 ab	35.7 ab	27.6 b	28.3 a
57353	6x	43.9 a	40.4 a	38.5 a	33.4 a	29.4 a
Prairie	6x	35.4 b	32.2 b	32.2 bc	28.9 b	28.3 a
Maku		20.7 d	19.4 e	19.9 e	14.8 d	13.8 c
Huia		17.5 d	21.0 de	28.1 cd	14.2 d	14.5 c
SLSD (5%)		5.14	5.37	5.40	3.93	3.43

Variety means within any environment with the same letter beside are not significantly different using Scheffe's-Least Significant Difference at the 5% level (SLSD(5%)).

As climatic and edaphic conditions became harsher, mean leaf length was found to decrease.

Leaflet Length-Width Ratio

The variety means for leaflet length-width ratio at all sites are presented in Table 6 (page 46). The prominent result of this table is that 51140 had the highest mean leaflet length-width ratio under all environmental conditions. An important but less obvious result is that the ranking of the *T. ambiguum* varieties remained constant for all environments. The ranking was, from round leaflets to oblate leaflets, Forest, Summit, Prairie, Treeline, 57353 and 51140. It is interesting to note that, although the diploids had rounder leaflets than the polyploids, there was no consistent difference between the tetraploids and hexaploids.

Huia had very round leaflets but under none of the experimental conditions were they significantly different from the two diploid *T. ambiguum* varieties. The leaflet length-width ratio of Maku was similar to that of Prairie under all conditions although the leaflets were shorter (Table 5, page 44).

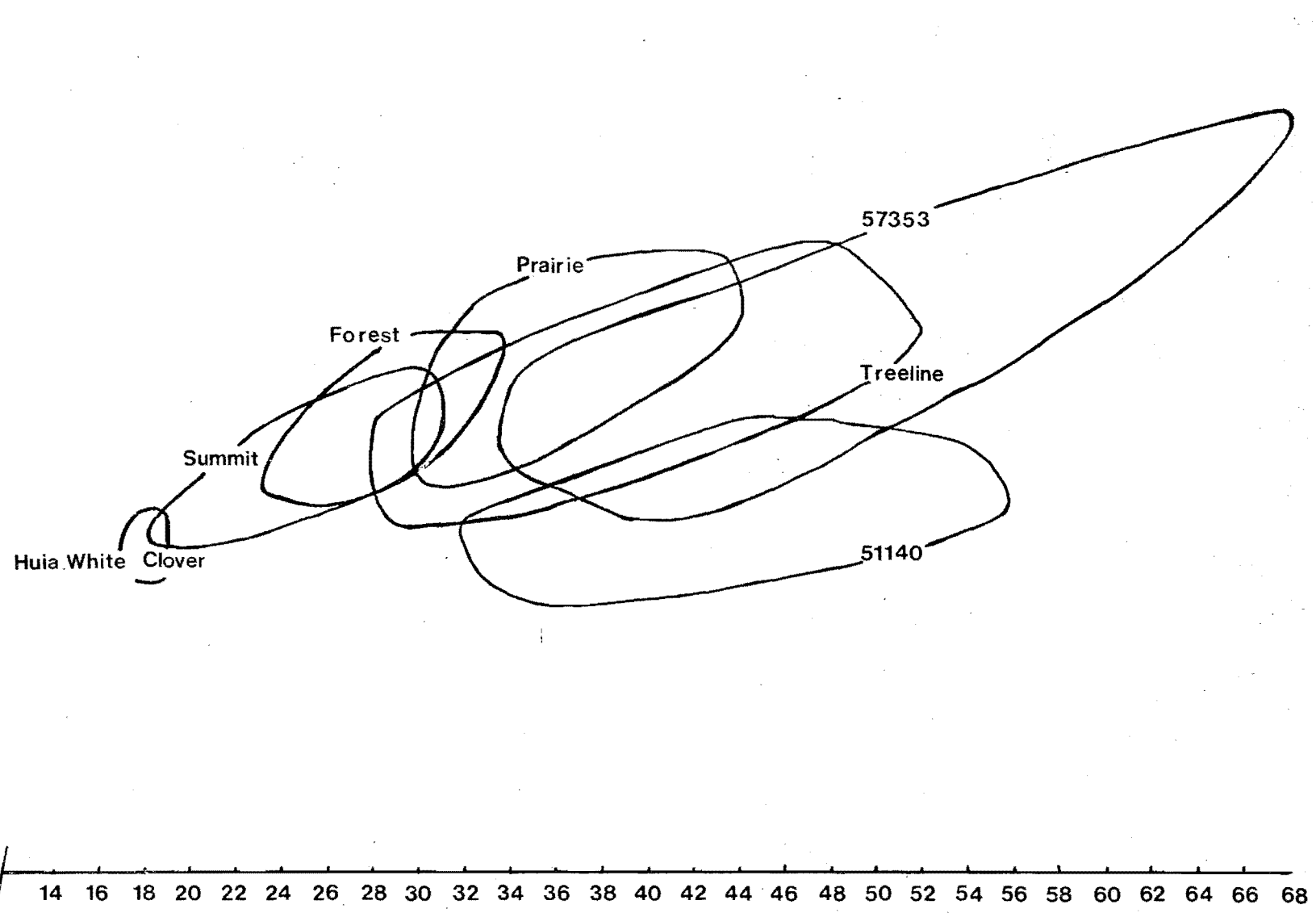
Figure 1 (page 47) presents the distribution of leaflet lengths and leaflet widths for genotypes within each variety when grown in Wakanui soil at the low altitude site. From this figure it is clear that, apart from leaflet size, 57353 contained genotypes of wide ranging leaf dimensions, while the diploids were more uniform. The other three polyploid varieties were intermediate in variability. Huia white clover was very uniform but this apparent uniformity may be due, at least in part, to the low number of genotypes sampled. The overlap among varieties of *T. ambiguum*, as apparent in this figure, appears to be typical of the majority of plant parameters measured in this experiment.

Table 6: Variety means for leaflet length : width ratio at all environments

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	1.40 cd	1.34 e	1.35 e	1.27 e	1.33 de
Summit	2x	1.43 c	1.37 de	1.36 c	1.39 de	1.36 de
51140	4x	2.62 a	2.61 a	2.62 a	2.57 a	2.66 a
Treeline	4x	1.81 b	1.73 bc	1.71 b	1.77 bc	1.99 b
57353	6x	1.97 b	1.92 b	1.82 b	1.98 b	1.94 b
Prairie	6x	1.56 c	1.59 cd	1.55 bc	1.63 c	1.67 c
Maku		1.50 c	1.62 c	1.53 b	1.56 cd	1.45 cd
Huia		1.23 d	1.15 e	1.26 c	1.15 e	1.17 e
SLSD (5%)		0.221	0.241	0.286	0.242	0.229

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Figure 1: Distribution of leaflet length verses leaflet width for plants grown in Wakanui soil at Lincoln College



Petiole Length

Table 7 (page 49) presents the variety means for petiole length at all experimental sites. From this table it is clear that Treeline generally had the longest petioles while the diploids, Forest and Summit, had the shortest under all conditions. The two hexaploids, 57353 and Prairie, and 51140 were generally intermediate between Treeline and the diploids.

The petiole length of Huia was not significantly different to Treeline at any of the sites.

Harsh environmental conditions depressed petiole length in all the varieties but the longer petioled varieties exhibited a greater depression. Huia responded to harsh environmental conditions in a similar way to Treeline although one would expect the less cold-tolerant Huia to have been more greatly affected by the harsh conditions.

Plant Height

The variety means for plant height in each environment are presented in Table 8 (page 50). It is clear from this table that the tetraploids, Treeline and 51140, were the tallest varieties while the diploids, Summit and Forest, were generally the shortest at all experimental sites. The hexaploid varieties, Prairie and 57353, were intermediate in height between the tetraploids and diploids but were, in general, not distinct from either of these two ploidy levels.

Maku was much taller than any of the *Trifolium* varieties at the three 'better' sites and equivalent in height to Treeline in the two 'harsher' sites. The tallness in 'easier' sites is brought about by the change in growth habit attributable to flowering. At the other two sites flowering had not occurred at the time of measurement one month before harvest.

Table 7: Variety means for petiole length at all environments (centimetres)

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	5.50 de	5.65 d	5.59 b	3.86 a	2.52 c
Summit	2x	4.86 e	6.11 cd	5.52 b	3.75 a	2.73 bc
51140	4x	7.63 bc	7.50 bc	7.42 b	4.93 a	3.55 a
Treeline	4x	9.31 a	10.13 a	9.83 a	4.94 a	3.94 a
57353	6x	8.50 ab	7.71 bc	7.51 b	5.11 a	3.35 ab
Prairie	6x	6.79 cd	6.21 cd	5.83 b	4.34 a	3.48 a
Maku		-	-	-	-	-
Huia		8.30 ab	8.80 ab	10.4 a	4.30 a	3.90 a
SLSD (5%)		1.48	1.80	1.99	1.79	0.74

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Table 8: Variety means for plant height at all environments (centimetres)

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	6.50 e	4.47 e	5.28 de	3.36 e	2.90 e
Summit	2x	6.88 de	4.80 de	5.11 e	3.43 de	2.98 e
51140	4x	12.07 bc	7.68 c	6.77 cd	4.77 bc	4.73 bc
Treeline	4x	14.30 b	10.50 b	9.26 b	5.22 b	5.24 ab
57353	6x	9.93 cd	5.54 de	5.86 de	4.55 bc	4.04 cd
Prairie	6x	8.17 de	4.98 de	5.12 e	4.26 cd	4.21 c
Maku		29.90 a	22.30 a	12.90 a	6.40 a	5.90 a
Huia		9.33 cde	6.70 cd	7.78 bc	3.25 e	3.33 de
SLSD (5%)		2.97	2.12	1.64	0.87	0.79

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Huia was shorter than Treeline under all environmental conditions and was depressed by harsher conditions in a manner similar to that for the *T. ambiguum* varieties.

Plant Height-Width Ratio

The variety means for height-width ratio at all experimental sites is presented in Table 9 (page 52). These ratios were calculated as indexes of growth habit. The tetraploids, Treeline and 51140, had the most erect growth habit while both the diploids and the hexaploids were more prostrate. Huia was the most prostrate as expected from its stoloniferous growth habit. Maku was erect at the lowland sites but became more prostrate as the environmental conditions became harsher.

In general, harsher environmental conditions made erect varieties more prostrate. At least part of this change in growth habit could be attributed to morphological changes caused by differing flowering responses.

Leaf Markings and Multiple Leaflets

The percentage of the 30 genotypes within each variety which had leaf marks are presented below:

Forest	0	
Summit	60	
51140	10	(indistinct when present)
Treeline	60	
57353	90	
Prairie	100	

These differences offer a possible means of distinguishing between varieties.

Leaves with more than three leaflets were observed in two of the six varieties. In 57353 two genotypes out of 50 were observed to have some leaves with greater than three leaflets. On these plants leaves with four, five and sometimes seven equal-sized leaflets were observed. The other variety

Table 9: Variety means for plant height : width ratio at all the environments

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	0.27 bc	0.29 bc	0.37 c	0.34 c	0.35 c
Summit	2x	0.35 b	0.33 b	0.40 bc	0.39 bc	0.35 c
51140	4x	0.53 a	0.47 a	0.53 ab	0.50 a	0.49 a
Treeline	4x	0.55 a	0.56 a	0.62 a	0.48 ab	0.47 ab
57353	6x	0.34 b	0.29 bc	0.43 bc	0.41 abc	0.40 bc
Prairie	6x	0.31 bc	0.30 bc	0.43 bc	0.39 bc	0.42 abc
Maku		0.51 a	0.49 a	0.45 bc	0.34 c	0.35 c
Huia		0.19 c	0.19 c	0.21 d	0.19 d	0.16 d
SLSD (5%)		0.118	0.124	0.146	0.115	0.082

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

which had genotypes producing a small proportion of leaves with greater than three leaflets was Treeline. In Treeline 20 out of 50 genotypes growing at Lincoln College in February 1978 had leaves with extra leaflets. Generally, within Treeline the leaves with extra leaflets occurred on daughter plants rather than on the main crown and the extra leaflets were usually much smaller than the normal three leaflets. The Treeline genotypes with extra leaflets produced leaves with five or seven leaflets and occasionally with four or six. It is likely that for both varieties the effect was genotypic in origin as clonal materal from these plants produced multiple leaflets at all five sites used in the experiment one.

One Treeline genotype had 10 percent of its leaves with multiple leaflets but, in general, most genotypes had less than one percent multiple leaflets.

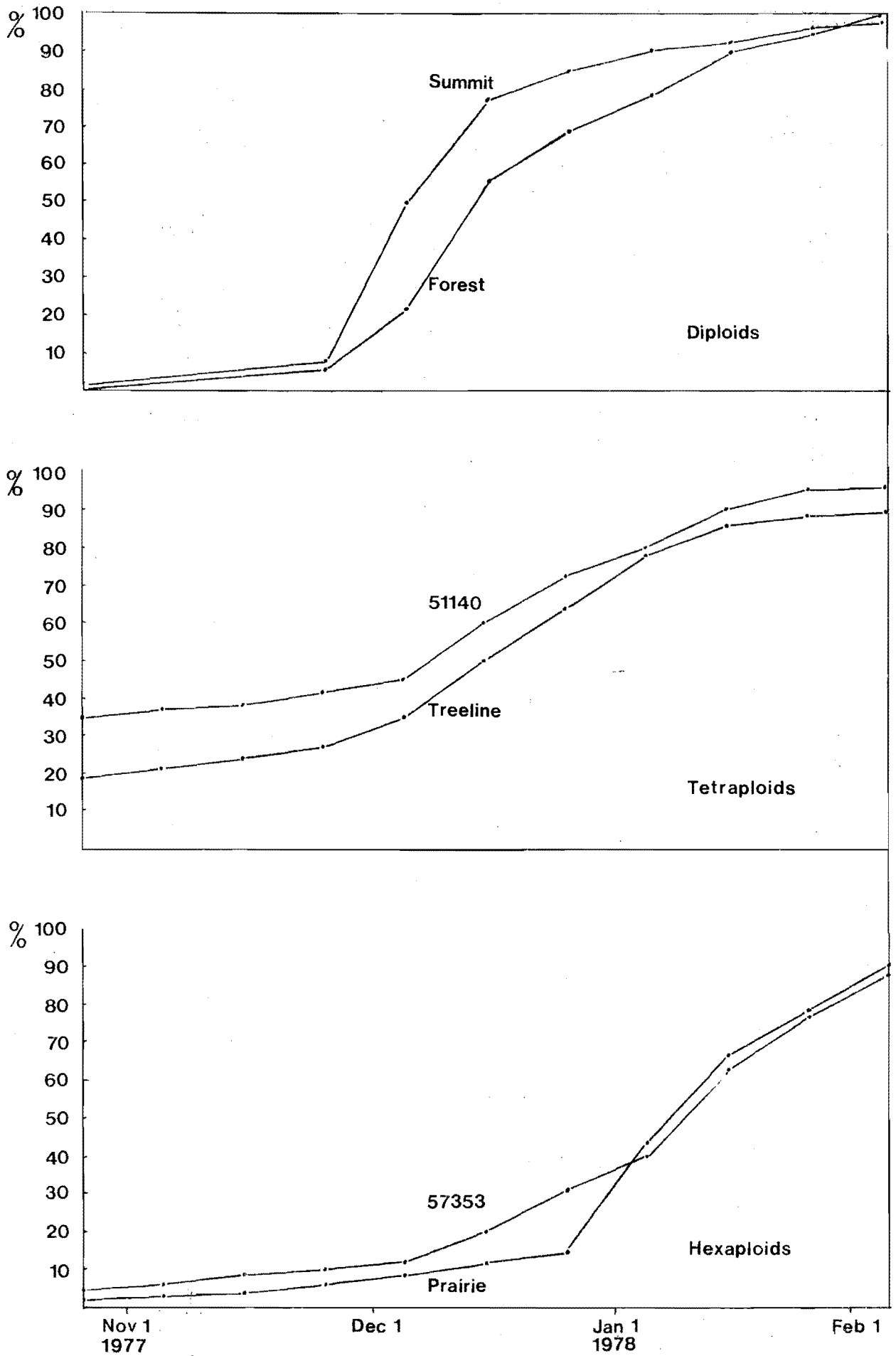
Outlines of multiple leaflets are presented in Appendix B.

Flowering Date

The cumulative flowering percentages from late October until early February for each variety growing in Wakanui soil at the low altitude site are depicted in Figure 2 (page 54). From this figure it is obvious that the three ploidy levels exhibited different flowering responses while both varieties with each ploidy level were similar. All three ploidy levels exhibited sigmoid curves typical of cumulative normal distributions. However, the mean and variance of these normal distributions were different.

The diploids started flowering at the end of November, peaked in mid-December and by mid-January most had initiated flowering. The initiation of flowering in the tetraploids was spread very widely over the season. Some

Figure 2: Cumulative flowering percentages of all varieties grown in Wakanui soil at Lincoln College



plants flowered before transplanting in mid-October while most plants initiated flowering between early December and mid-January. There were still some tetraploids which had not flowered at harvest in mid-March. The hexaploids initiated flowering much later than either the diploids or the tetraploids. A few hexaploid plants had flowered by mid-December but most initiated flowering in January while a few were later. At the harvest in mid-March all the diploids had flowered, 98 and 97 percent of the two tetraploids varieties, 51140 and Treeline, respectively, had flowered while 97 and 92 percent of the two hexaploid varieties, Prairie and 57353 respectively, had flowered (Table 10, page 56).

From Table 10 (page 56), presenting the percentage of plants within each variety which had flowered at some stage over the season for all the environments, it is apparent that under all the conditions used, flowering became later with increasing ploidy level.

The mean date of flowering in the Wakanui soil at low altitude was 11th November for Huia while that for Maku was 13th December. The variation in the date of floral initiation for Maku and Huia was considerably less than for any of the *T. ambiguum* varieties. All the Huia flowered within 3 weeks while all the Maku flowered within 2 weeks. The lower variance in Huia and Maku may be due in part to having few genotypes but it was most likely low compared with *T. ambiguum* because of the higher genetic diversity within the *T. ambiguum* varieties.

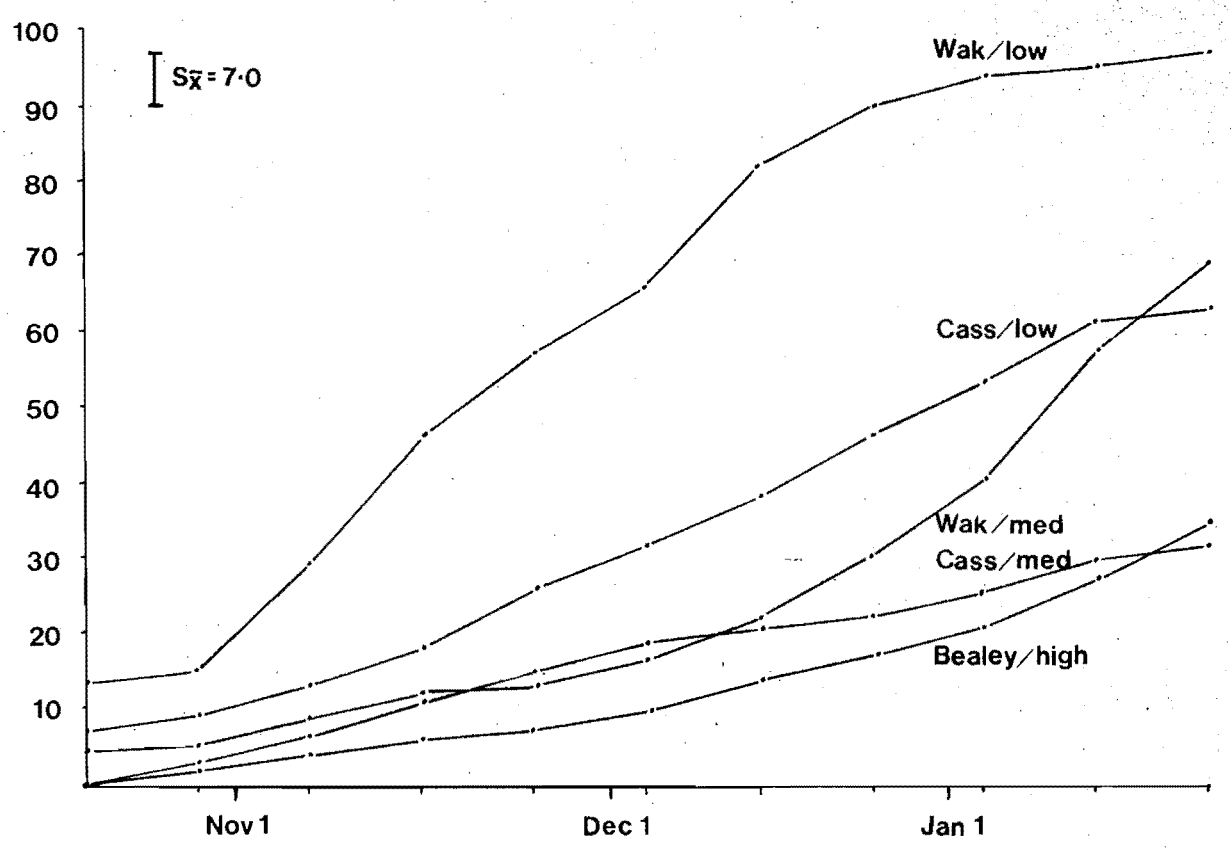
Figure 3 (page 57) presents the mean cumulative flowering percentages for all five environments. From this figure it is clear that the harsher environments caused flowering to be delayed. However, it should also be noted that the Wakanui soil at low altitude was transplanted a month earlier

Table 10: The percentage of plants within each variety which had flowered at some stage over the season at all environments

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	100	78	83	62	52
Summit	2x	100	90	93	79	71
51140	4x	98	70	83	54	43
Treeline	4x	97	67	83	41	43
57353	6x	92	42	57	31	28
Prairie	6x	97	37	63	30	22

No significance test possible as these were unreplicated results.

Figure 3: **Cumulative flowering percentages at all five environments (mean of six varieties)**



than the other sites, which themselves could be considered comparable. Even taking this effect into account, there was still a delay in flowering at the high altitude site and a lesser delay in flowering at the medium elevation sites.

Production of Flowerheads

The mean number of flowerheads per flowering plant for each variety at each site is presented in Table 11 (page 59). The only significant difference was that Summit had more flowers than 57353 when grown in Cass soil at low altitude. It is also noticeable that the mean weight per flowerhead for 57353 at this site was 0.17 g while that for Summit was 0.11 g. Considering the difference in individual flowerhead weight, Summit plants produced nearly twice the mass of flowerheads than did 57353, 1.16 g compared with 0.65 g. Although 57353 had the heaviest individual flowerheads Summit did not have the smallest, the smallest were Treeline with a mean weight of 0.09 g at this site. Whether these weight differences were caused by differences in floret number or floret size was not determined in this study. The reason why Summit produced more flowerheads than 57353 was most probably due to the earlier flowering of Summit allowing a longer period for formation of flowerheads.

Above Ground Dry Weight

Table 12 (page 60) presents the mean above ground dry weight relative to Treeline at each site. Treeline was chosen for the standard as this promising variety tended to be the most productive at all sites. The mean above ground dry weights of Treeline are also given in this table.

It can be seen from this table that the performance of 51140 was poor at all sites, generally 30 to 40 percent below Treeline. The hexaploid varieties were generally lower yielding than Treeline but these differences

Table 11: Variety means for the number of flowerheads per flowering plant at all environments

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	35.95 a	7.15 ab	10.61 a	2.82 a	2.35 a
Summit	2x	31.57 a	10.54 a	12.31 a	3.23 a	3.06 a
51140	4x	41.80 a	7.74 ab	9.08 a	3.22 a	1.96 a
Treeline	4x	40.27 a	5.67 ab	9.45 a	2.78 a	2.08 a
57353	6x	35.62 a	3.85 b	8.24 a	1.37 a	2.33 a
Prairie	6x	42.16 a	7.68 ab	6.76 a	1.65 a	2.33 a
SLSD(5%)		18.95	4.94	7.18	2.06	2.01

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Table 12: Above ground dry weights relative to c.v. Treeline, variety means at all environments

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low *	Cass/low *	Wak/med	Cass/med	Bealey/high
Forest	2x	68 cd	64 d	96 bc	96 c	69 bc
Summit	2x	50 d	68 d	90 bc	100 c	85 bc
51140	4x	71 cd	60 d	68 c	71 c	59 c
Treeline	4x	100 c	100 c	100 bc	100 c	100 b
57353	6x	98 c	77 cd	88 bc	89 c	73 bc
Prairie	6x	85 cd	71 cd	74 c	86 c	73 bc
Maku		386 b	545 b	135 b	253 b	289 a
Huia		595 a	744 a	615 a	305 a	267 a
SLSD (5%)		36	29	56	36	31
Treeline mean (g)		18.74	5.17	6.57	1.60	1.40

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

* flowers not included (Vegetative top dry weights).

were not significant. Similarly, the diploid varieties were generally 30 to 50 percent lower yielding than Treeline although they both performed relatively well at the medium elevation sites.

The ploidy level had no apparent affect on herbage production although it was expected that the diploids, having evolved under high altitude conditions, would perform relatively better at the high altitude site. The relatively poor performance of the diploids may have been due to a lower level of nitrogen fixation rather than poor adaptation to the conditions. This remains unconfirmed as nitrogen fixation was not studied in this trial.

Both Maku and Huia yielded significantly more than any of the *T. ambiguum* varieties at all sites, except for Maku at the medium elevation site in Wakanui soil. This low yield is unexpected and is possibly due to the location of Maku near the edge of the trial plot. In general, the harsher the environment the better *T. ambiguum* performed relative to Maku and Huia.

Rhizome Dry Weight

The mean rhizome dry weights for each variety, relative to Treeline, are presented in Table 13 (page 62) along with the mean rhizome dry weight of Treeline. It is clear that both Prairie and Treeline produced a significantly higher yield of rhizomes at all sites than did Summit. No significant differences were observed between Prairie and Treeline at any of the sites. At all sites the other three varieties, 57353, 51140 and Forest were intermediate between the higher producing, Prairie and Treeline and the consistently lowest producing, Summit. However, the ranking of 57353, 51140 and Forest was not consistent among the environments.

Table 13: Rhizome dry weights relative to c.v. Treeline, variety means at all environments

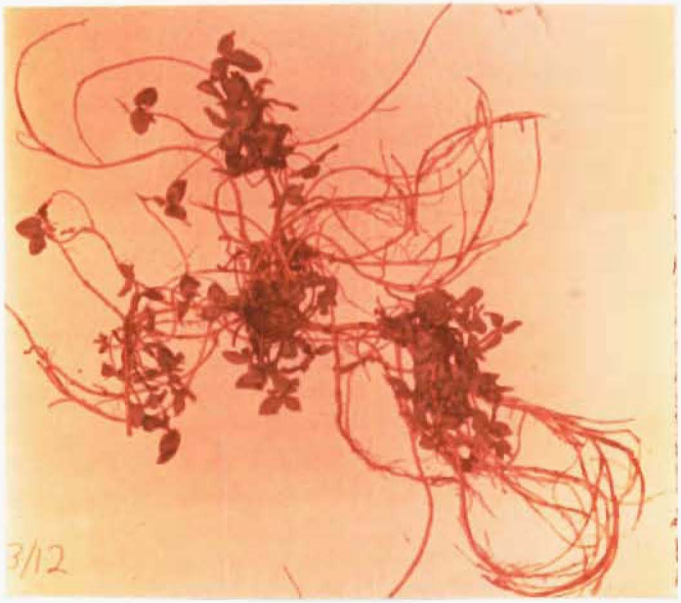
Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Summit	2x	45 cd	41 bc	85 ab	99 ab	60 ab
Forest	2x	18 d	15 c	26 b	44 c	24 b
51140	4x	57 bcd	50 bc	45 ab	73 bc	70 ab
Treeline	4x	100 ab	100 a	100 a	100 ab	100 a
57353	6x	75 bc	47 bc	44 ab	80 bc	69 ab
Prairie	6x	122 a	71 ab	107 a	144 a	100 a
SLDS (5%)		43	37	73	49	56
Treeline mean (g)		13.07	7.31	1.93	1.39	1.01

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Plate 2. Poorly Rhizomatous 'Summit' Plant

A poorly rhizomatous 'Summit' plant with prostrate growth habit grown in Cass soil at low altitude. This plant had four rhizomes with a maximum length of 7 cm and its total dry weight (18.18 g) consisted of 31 percent vegetative top growth, 0.5 percent rhizome, 66 percent root and 2.5 percent flowers. The top growth on this plant represents two weeks regrowth after cutting in early March and not the total seasonal herbage production.

Plate 3. Typical 'Prairie' Plant



A 'Prairie' plant with average rhizome production grown in Cass soil at low altitude. This plant had 14 rhizomes, the longest was 45 cm and its total plant dry weight (16.20 g) consisted of 20 percent vegetative top growth, 33 percent rhizome, 46 percent root and 1 percent flowers. The top growth on this plant represents two weeks regrowth after cutting in early March and not the total seasonal herbage production.

Plate 4. Erect 'Treeline' Genotype

Two poorly rhizomatous erect 'Treeline' plants of the same genotype grown in Cass soil at low altitude. The plant on the left had 4 rhizomes with a maximum length of 18 cm and its total plant dry weight (22.86 g) consisted of 27 percent vegetative top growth, 1.5 percent rhizomes, 71 percent root and 0.5 percent flowers. The plant on the right had 3 rhizomes with a maximum length of 13 cm and its total plant dry weight (26.87 g) consisted of 32 percent vegetative top growth, 1 percent rhizomes, 65 percent root and 2 percent flowers. The top growth on these plants represent two weeks regrowth and not the total seasonal herbage production.

Plate 5. Highly Rhizomatous '57353' Plant

A highly rhizomatous '57353' plant grown in Cass soil at low altitude. This plant had 9 rhizomes with a maximum length of 90 cm and its total plant dry weight (14.77 g) consisted of 23 percent vegetative top growth, 48 percent rhizomes, 26 percent roots and 3 percent flowers. The top growth on this plant represents two weeks regrowth after cutting in early March and not the total seasonal herbage production.

No consistent ploidy effects were noticeable for rhizome dry weights and for each ploidy level the two varieties were significantly different in at least one environment. Forest was significantly more productive than Summit when grown in Cass soil at the medium altitudes, Treeline was significantly better than 51140 when grown in Cass soil at the low altitude site and Prairie produced a significantly greater rhizome mass than 57353 at both the low altitude site in Wakanui soil and the medium elevation site in Cass soil.

The varieties differed in the number of plants which produced rhizomes. The percentage of plants producing rhizomes within each variety at all sites is presented in Table 14 (page 68). The variety differences were particularly noticeable in the harsh high altitude environment where only 61 percent of Summit plants produced rhizomes compared with 97 percent for Prairie. In the other four varieties, Treeline, Forest, 51140 and 57353, 81, 88, 93 and 86 percent respectively grew rhizomes under these conditions. Under the favourable conditions of the Wakanui soil at the low altitude site, over 95 percent of plants within each variety produced rhizomes. The absence of rhizomes within each variety under harsh environmental conditions did not appear to be genotypic in origin, because within most genotypes, plants with and others without rhizomes were found.

Rhizome Dry Weight Proportion

Table 15 (page 69) presents the variety means for proportion of total plant dry weight consisting of rhizomes at each site. Prairie consistently had the highest proportion of rhizome dry weight at all sites while Summit had the lowest. The difference between these two was significant at all sites. At both the medium elevation sites, the rhizome dry weight proportion of Treeline was depressed to a significantly lower level than Prairie. However,

Table 14: Percentage of plants within each variety which produced rhizomes, at all environments

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	100	98	81	91	88
Summit	2x	95	91	59	77	61
51140	4x	100	100	70	80	93
Treeline	4x	100	96	72	83	81
57353	6x	98	96	61	80	86
Prairie	6x	98	100	91	100	97

No significance test possible as these were unreplicated results.

Table 15: Proportion of total plant dry weight which was rhizome dry weight, variety means at each environment

Variety Ploidy	Environment (Soil/Altitude)					
	Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high	Mean $\bar{X}$..
Forest	.166 bc	.268 ab	.140 ab	.263 ab	.187 a	.205 bc
Summit	.077 c	.094 c	.044 c	.131 c	.070 b	.083 d
51140	.174 b	.278 ab	.079 bc	.208 bc	.173 ab	.182 b
Treeline	.236 ab	.336 ab	.109 bc	.221 bc	.175 ab	.215 b
57353	.195 b	.238 b	.064 bc	.194 bc	.166 ab	.171 c
Prairie	.319 a	.377 a	.206 a	.349 a	.241 a	.298 a
SLSD(5%)	.096	.126	.086	.112	.106	.0381

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at 0.95 probability (SLSD(5%)).

at the high altitude site the proportion of rhizome dry weight in Prairie was also depressed, causing it to be not significantly greater than in Treeline.

Forest also had a relatively high proportion of rhizome dry weight and was not significantly lower than in Prairie at four out of the five sites. At the remaining site, Wakanui soil at low altitude, Forest had a significantly lower proportion than did Prairie.

Ploidy level effects did not appear to be important. Forest was found to have a significantly higher proportion of rhizomes at all sites than did Summit. Similarly, Prairie had a greater proportion than 57353 at all sites except the high altitude site. However, Treeline and 51140 did not differ significantly at any of the sites.

The mean over all sites shows clearly that Prairie had the greatest proportion of rhizomes while Treeline, 51140 and Forest all had a lower proportion and were not significantly different from each other. Forest was not significantly higher than 57353, while all the varieties had a significantly higher proportion than Summit.

The environmental effect was highly significant and from Table 15 (page 69) it is clear that plants grown in the Cass soil had a much higher proportion of rhizomes than when grown in Wakanui soil at the same location. This is most likely due to the lower bulk density of the Cass soil and will be discussed in more detail later.

Number of Rhizomes

Table 14 (page 71), presents the mean number of rhizomes for each variety at all sites. Clearly shown in this table is the absence

Table 16: Number of rhizomes, variety means at all sites

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	17.9 abc	8.6 ab	7.4 a	7.2 a	4.6 ab
Summit	2x	10.5 c	4.7 b	3.1 bc	4.4 bc	2.5 b
51140	4x	15.7 bc	6.3 b	2.9 bc	3.0 c	3.4 b
Treeline	4x	25.6 a	11.2 a	6.3 ab	5.8 ab	4.9 ab
57353	6x	12.6 c	5.4 b	2.1 c	3.3 bc	2.6 b
Prairie	6x	23.7 ab	10.7 a	6.2 ab	7.7 a	6.4 a
SLSD(5%)		8.48	3.89	3.98	2.59	2.54

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

of ploidy level effects. Prairie had significantly more rhizomes than 57353 at all sites while at both the medium altitude sites Forest had significantly more than Summit. Similarly, Treeline had significantly more than 51140 at both low altitude sites and in the Cass soil at medium elevation. Treeline, Prairie and Forest, the three varieties with the highest number of rhizomes, did not differ significantly at any site. Similarly, 57353, 51140 and Summit did not differ significantly.

Rhizome number was found to decrease with harsh edaphic and climatic conditions in a similar manner to that for rhizome length, exhibiting a noticeable depression in the Wakanui soil at medium elevation. This was most likely due to the high bulk density and compaction of this soil.

Rhizome Length

The mean rhizome length of the longest rhizome on each plant with rhizomes for each variety grown at all environments are presented in Table 17 (page 73). From this table it can be seen that in conditions that were favourable for the production of long rhizomes the mean rhizome length increased with increasing ploidy level. The two varieties within each ploidy level were not significantly different at any of the experimental sites. At sites which restricted rhizome length, such as Wakanui soil at medium altitude, potential differences between ploidy levels were not expressed. In this case the restriction was most likely caused by the high density of the soil (BD = 1.5 - 1.6) and compaction when dry.

Rhizome Characteristic in the Two Soils

Table 18 (page 74) presents the variety means for internode length, number of nodes and the proportion of branching nodes in the two soils at medium elevation. From this table it can be seen that both the number of

Table 17: Lengths of longest rhizome, variety means at all environments (centimetres) (corrected for plants with rhizomes)

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	24.6 cd	28.6 bc	16.7 a	25.8 ab	17.6 a
Summit	2x	17.0 d	22.3 c	13.4 a	22.3 b	13.3 a
51140	4x	26.0 bc	38.0 ab	13.7 a	22.3 b	17.4 a
Treeline	4x	27.7 bc	36.1 ab	14.2 a	22.8 b	16.7 a
57353	6x	32.9 ab	42.7 a	13.3 a	33.4 a	19.1 a
Prairie	6x	37.2 a	42.4 a	16.9 a	27.6 ab	18.2 a
SLSD(5%)		7.9	10.8	6.2	9.4	6.3

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Table 18: Rhizome characteristics in the two soils, variety means of internode lengths, number of nodes and the proportion of branching nodes on the longest rhizome (Medium altitude)

	Number of Nodes		Mean Internode Length (mm)		Proportion of Branching Nodes	
Soil	Wakanui	Cass	Wakanui	Cass	Wakanui	Cass
Variety						
Forest	12.7 a	15.3 a	12 ab	16 cd	.43 ab	.29 a
Summit	11.9 ab	14.0 ab	10 b	15 d	.28 b	.27 a
51140	10.4 bc	10.3 c	12 ab	20 bc	.43 ab	.33 a
Treeline	9.6 cd	10.6 c	13 ab	20 bc	.54 a	.40 a
57353	7.7 d	11.9 bc	15 a	26 a	.34 ab	.25 a
Prairie	10.6 ab	11.3 c	15 a	22 ab	.40 ab	.35 a
SLSD(5%)	2.2	2.4	3	4	.25	.22

Variety means of plants grown in any soil for any characteristic with the same letter beside are not significantly different using Scheffe's Least Significant Difference at 0.95 probability (SLSD(5%)).

nodes and mean internode length were higher in the Cass soil. The mean number of nodes was 17 percent higher in the Cass soil while the mean internode length was 55 percent longer. Therefore, the 75 percent increase in rhizome length was predominantly attributable to longer internodes although the number of nodes contributed a small amount to the increase. These differences between the two soils were probably due to bulk density differences, the Cass soil was 0.7 to 0.8 while the Wakanui was 1.5 to 1.6. The physical restrictions imposed on rhizome growth by the Wakanui soil may have been extremely high as this soil was observed to become extremely hard and compact when dry.

Both varieties within each ploidy level had a similar number of nodes when grown in the Cass soil. When grown in the Wakanui soil the two varieties responded differently to the restrictive edaphic conditions. Generally, in the unrestrictive conditions of the Cass soil, the diploids had the most nodes while the tetraploids had the least, the hexaploids were intermediate and not significantly different to the tetraploids.

Mean internode lengths were similar for both varieties within each ploidy level when grown in either of the two soils. The mean internode length was found to increase with ploidy level. However, the three ploidy levels were not distinct as both a diploid and a hexaploid variety were not significantly different from the tetraploid varieties when grown in the Cass soil.

The proportion of branching nodes was significantly higher in the Wakanui soil than in the Cass soil. This was most likely due to the better nutritional status of the Wakanui soil (Appendix A), most probably nitrogen. McIntrye (1972) found that nitrogen level was a very important factor

associated with apical dominance of the rhizome system of *Agropyron repens*. However, Phillips (1969) reported that other nutrients can effect apical dominance in general. If *T. ambiguum* was effectively nodulated then nitrogen fixation would have tended to equalise the nitrogen status of plants grown in the two soils. Even though nodulation was not studied in this experiment the lower branching in the Cass soil may be an indication that root nodulation was not very effective in the present study.

In the Wakanui soil, Treeline had significantly greater branching than Summit. However, any other potential differences among varieties were masked by the very high variability (CV% = 84) within genotypes. For example, 57353 had significantly less branching than Treeline in the Wakanui soil when calculated at the 10 percent probability level but not at the 5 percent level.

Number of Daughter Plants

The mean number of daughter plants for each variety grown at all sites are presented in Table 19 (page 77). From this table it can be seen that when the plants were grown in either of the low altitude sites, Treeline had significantly more daughter plants than Forest, 57353 and Summit. The varieties Prairie and 51140 were intermediate between these two groups. In the Wakanui soil at this location, Prairie also had a significantly high number of daughter plants than 57353 and Summit. However, at the medium elevation sites, the variety means were not significantly different. At the high altitude site, where plants generally produced the fewest daughter plants, Prairie produced significantly more than Summit. Considering Summit's reputation as a subalpine form of *T. ambiguum* (Barnard, 1972) this result was unexpected.

Table 19: Number of daughter plants, variety means at each environment

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	5.72 bc	1.28 b	1.17 a	0.93 a	0.36 ab
Summit	2x	2.82 c	0.95 b	0.41 a	0.36 a	0.16 b
51140	4x	7.10 abc	1.92 ab	0.68 a	1.05 a	0.73 ab
Treeline	4x	10.41 a	3.83 a	0.94 a	0.74 a	0.74 ab
57353	6x	4.80 c	1.25 b	0.59 a	0.79 a	0.55 ab
Prairie	6x	9.79 ab	2.17 ab	0.95 a	1.12 a	0.84 a
SLSD(5%)		4.43	1.91	0.79	0.86	0.67

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Ploidy level effects obviously had a minimal effect on the number of daughter plants produced. There was no apparent trend for the number of daughter plants to increase with ploidy level under any of the experimental conditions.

Root Dry Weight

Table 20 (page 79) presents the mean dry weight of roots for each variety relative to Treeline in all environments. The mean root dry weights of Treeline are also given. From this table it is apparent that Treeline had a greater root mass than all the varieties except 57353. The other four varieties, Forest, Summit, 51140 and Prairie were generally lower, but their rankings were not consistent throughout the environments.

No ploidy level effects were observed for root weight as the varieties within each ploidy level were dissimilar and within the range of the other ploidy levels.

The root dry weights of Huia and Maku ranged from higher than Treeline to lower than the poorest *T. ambiguum* variety depending on the environmental conditions. Their root dry weights (Table 12 page 60) and the proportion of the plant consisting of root dry weight (Table 21 page 80).

Proportional Root Dry Weight

Table 21 (page 80) presents the variety means at all sites for the proportion of total plant dry weight contributed by the roots. The results show that Prairie had the lowest proportion of roots for the *T. ambiguum* varieties, but this was not significantly different from Forest under any conditions. In general, the other four varieties, Summit, 51140, Treeline and 57353 had higher proportions regardless of environmental conditions.

Table 20: Root dry weights relative to c.v. Treeline, variety means at all environments

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	54 c	66 c	68 b	72 c	58 bc
Summit	2x	50 c	71 bc	59 b	75 bc	68 b
51140	4x	66 bc	74 bc	61 b	68 c	80 ab
Treeline	4x	100 a	100 ab	100 a	100 ab	100 a
57353	6x	94 ab	92 bc	76 ab	96 abc	84 ab
Prairie	6x	61 c	68 bc	57 b	73 bc	73 ab
Maku		120 a	129 a	26 c	105 a	57 bc
Huia		53 c	100 ab	62 b	72 bc	37 c
SLSD (5%)		31	32	29	28	29
Treeline mean (g)		20.4	7.8	8.4	3.4	3.3

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Table 21: Variety means for the proportion root dry weight at all sites

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	0.32 ab	0.42 ab	0.42 b	0.45 b	0.54 a
Summit	2x	0.39 a	0.51 a	0.44 b	0.54 a	0.60 a
51140	4x	0.35 a	0.45 ab	0.52 a	0.52 ab	0.63 a
Treeline	4x	0.36 a	0.40 b	0.51 ab	0.53 ab	0.59 a
57353	6x	0.36 a	0.48 a	0.55 a	0.57 a	0.61 a
Prairie	6x	0.25 b	0.36 bc	0.45 b	0.42 bc	0.54 a
Maku		0.25 b	0.26 cd	0.20 c	0.46 b	0.32 b
Huia		0.09 c	0.17 d	0.11 c	0.33 c	0.25 b
SLSD (5%)		0.073	0.100	0.092	0.111	0.097

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

The low root dry weight proportion observed for Prairie may have been caused by its low root vigour at transplanting (Table 2 page 40). However, it is more likely that both these measurements reflect that Prairie had a relatively small root system compared with Treeline. It is interesting that Prairie had the largest proportion of rhizome dry weight. This may indicate that Prairie has developed a vigorous rhizome system at the expense of its root system.

No ploidy level effects were apparent for the root dry weight proportions as there were few significant or consistent effects observed.

Huia had a significantly lower proportion of root dry weight than all the *T. ambiguum* varieties. Similarly, Maku was lower than the *T. ambiguum* varieties but this difference was not significant under some environmental conditions.

Total Plant Dry Weight

The mean total plant dry weights for each variety relative to those of Treeline at each environment are given in Table 22 (page 82). The mean Treeline dry weights are also given. Of all the *T. ambiguum* varieties Treeline was consistently the highest yielding. Prairie ranged from 9 to 31 percent poorer than Treeline depending on the conditions while 57353 ranged from 5 to 28 percent poorer. The diploids and the other tetraploid variety were generally the poorest, ranging from 16 to 53 percent poorer than Treeline.

Despite these differences ploidy level still appeared to have little effect on total plant dry weight.

Under favourable environmental conditions Huia and Maku produced a higher total plant dry weight than all the *T. ambiguum* varieties. However,

Table 22: Total plant dry weight, variety means relative to c.v. Treeline at each environment

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	62 de	59 d	81 b	84 bc	61 c
Summit	2x	47 e	53 d	67 b	75 c	65 c
51140	4x	71 cde	64 d	62 b	70 c	73 bc
Treeline	4x	100 c	100 c	100 b	100 ab	100 ab
57353	6x	95 c	72 d	77 b	90 bc	79 abc
Prairie	6x	90 cd	70 d	69 b	91 bc	78 abc
Maku		171 b	186 b	66 b	119 a	105 a
Huia		215 a	225 a	270 a	115 a	88 abc
SLSD (5%)		29	24	44	23	27
Treeline mean (g)		56.7	20.6	16.9	6.4	5.7

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

under harsh conditions there were no significant differences between the highest yielding *T. ambiguum*, Treeline, and either Huia or Maku. The poor performance of Maku in Wakanui soil at intermediate elevation probably occurred because it grew near the edge of the plot and was subjected to weed competition and/or water stress.

Genotypic Coefficients of Variation

The genotypic coefficients of variation were calculated to determine the genetic variation within each variety. Table 23 (page 84) provides the mean genotypic coefficients of variation of a range of plant characteristics for each variety. Within any variety genetic variation was dependent on the plant characteristic measured. For example, in Treeline the genotypic coefficient of variation ranged from 17 percent for leaflet length to 80 percent for rhizome dry weight. In terms of potential for selection there were large differences between varieties for given plant characteristics. For example, rhizome dry weight exhibited genotypic coefficients of variation ranging from 16 percent in Summit to 80 percent in Treeline. However, for total plant dry weight the range was lower, from 26 percent in Summit to 42 in Treeline.

In general, Treeline was the most variable population, while 51140, 57353 and Prairie were intermediate, and Forest and Summit were the least variable. A notable feature is that the polyploid varieties had a consistently greater genotypic coefficient of variation than the diploid populations. This may be due to more intense selection in the diploids, as in Summit (Barnard, 1972), or to the greater potential for genetic segregation and recombination in the polyploids.

Table 23: Genotypic coefficients of variation for each variety, mean of all environments

	Forest	Summit	51140	Treeline	57353	Prairie
Rhizome length	28	23	39	31	39	31
Number rhizomes	54	26	35	59	29	41
Rhizome D.W.	40	16	47	80	42	58
Root D.W.	38	32	46	57	56	46
Above Ground D.W.	42	48	49	58	56	49
Total D.W.	27	26	39	42	41	39
Plant height	20	18	38	44	32	28
Petiole length	18	16	45	35	34	21
Leaflet length	10	8	21	17	20	11
Leaf area *	17	14	28	29	44	25
Height/width ratio	21	20	42	41	32	38
Mean	29	22	39	45	39	35

* Mean of 2 low altitude environments

Broad Sense Heritability Estimates

Broad sense heritability estimates for a wide range of plant characteristics, together with the standard error of the estimate, are presented in Table 24 (page 86). In general, morphological characteristics had the highest heritabilities, from 35 to 70 percent, while total plant yield and its components had medium heritabilities, from 16 to 32 percent. The number and dry weight of flowers exhibited the lowest heritabilities, from 7 to 12 percent. However, there were a large number of interesting specific heritabilities which require explanation.

Plant width would presumably be considered a morphological characteristic but the heritability estimate of 21.5 percent is lower than those of the morphological characteristics. This could be because plant width was highly correlated with above ground dry weight (r_G = 0.7) and was more a reflection of plant yield rather than any inherent morphological characteristics. This will be discussed in more detail later.

The date of flowering at low altitude in Wakanui soil had a heritability of 31.9 percent. For a species which exhibits a high correlation (r = 0.8) in flowering date between years (Townsend, 1970) this heritability estimate was lower than expected. This may reflect the use of only two replicates, as well as the possibility that the plants were too small to flower when photoperiodic conditions were conducive. If early-season photoperiod conditions could not induce flowering because of inadequate plant age or size, the heritability estimate may simply be a reflection of plant age or size.

Both flower dry weight and the number of flowers exhibited a very large environmental effect and genotype-environment interaction. This had the effect of lowering the heritability estimate. It was so low as to be negligible. The massive environmental effect on flowering was reflected in

Table 24: Broad sense heritability estimates

Characteristic	h_B^2 %	SE
Leaflet length/width ratio	68.3	2.9
Leaf weight	59.7	5.4
Leaflet length[2]	57.0	3.5
Leaf area[1]	50.4	6.0
Petiole weight[1]	47.7	6.1
Plant height	47.3	3.7
Weight/length petiole[1]	46.1	6.2
Leaflet width	45.5	3.7
Weight/leaf area[1]	42.7	6.3
Rhizome internode length[2]	40.2	7.9
Plant height/width ratio	34.9	3.6
Flowering date[3]	31.9	1.0
Above ground vegetative dry weight[2]	31.5	6.7
Root dry weight	29.0	3.5
Number of rhizomes	28.7	3.5
Petiole length	28.6	3.5
Length of longest rhizome	28.3	3.3
Proportion rhizome dry weight	27.9	3.4
Rhizome dry weight	27.8	3.5
Total plant dry weight	27.5	3.4
Proportion flower dry weight[1]	25.7	6.4
Number of nodes on longest rhizome[2]	23.9	8.0
Proportion above ground dry weight	23.9	3.3
Proportion root dry weight	23.9	3.3
Proportion vegetative top dry weight[1]	21.9	6.5
Plant width	21.5	3.2
Proportion of rhizome nodes branching[2]	16.7	6.8
Above ground dry weight (includes flowers)	16.4	2.9
Number of flowers	11.8	2.6
Number of daughter plants	11.4	2.6
Dry weight of flowers[1]	6.9	5.7

1 Measured only at the 2 low altitude environments
2 Measured only at the 2 medium altitude environments
3 Calculated only for Wakanui soil at low altitude

the total seed yields at the low altitude site. Plants grown in Wakanui soil produced a total of 522 g of seed, while those in the Cass soil produced only 16.5 g.

Above ground dry weight had a heritability of 16.4 percent while vegetative above ground dry weight (without flowers) had a heritability of 31.5 percent. This difference was probably due to the estimation of vegetative above ground dry weight in only two environments causing a much lower estimate of genotype-environment interaction variance. This low estimate would have inflated the genotypic variance and consequently the heritability estimate. Also, the large environmental effect on flower dry weight would have increased the phenotypic variance of the above ground dry weight and consequently decreased the heritability estimate.

The estimate of heritability for the proportion of branching nodes on the longest rhizome, calculated at 16.7 percent, may be low because of the large variation in apical dominance between different rhizomes on a single plant. This suggestion is reinforced by the higher heritability value calculated for weight per rhizome per unit length of 32.1 percent, which would be expected to be a similar indication of apical dominance. Additional consistency is indicated by its high correlation (r_G = 0.63) with the proportion of branching nodes.

Phenotypic and Genotypic Correlations

The matrix of phenotypic and genotypic correlations is provided in Appendix D. For all the phenotypic correlations calculated in five environments, all correlations greater than $\pm$ 0.3 were significant, while for genotypic correlations there was no simple significance test available. However, all genotypic correlation greater than $\pm$ 0.3 had a significant

covariance by the F test in the analysis of covariance.

To comprehend the correlation matrix, factor analysis was performed to group together plant characteristics. The only variable not included in the factor analysis was flowering date in which there were few correlations greater than 0.3 and these were with rhizome dry weight (r_G = 0.36), proportion above ground dry weight (r_G = -0.42) and proportion rhizome dry weight (r_G = 0.39). These correlations would indicate that rhizomatous plants tended to be later flowering and that such plants tended to have a lower proportion of their total dry weight above the ground.

Factor Analysis

Factor analysis was performed on the genotypic correlation matrix to aid comprehension of the relationships between plant characteristics. The first four factors of the analysis were able to explain 76 percent of the total variance present in the 25 plant characteristics of the correlation matrix. The first factor, which grouped together characteristics which were associated with plant size, explained 28 percent of the total variance. The second factor grouped together rhizome characteristics and contrasted these with both the proportion of root dry weight and proportion of above ground dry weight. This factor explained 22 percent of the variance. Morphological characteristics were grouped together in the third factor, explaining 18 percent of the variance. In the fourth factor, which accounted for 8 percent of the variance, the proportion above ground dry weight and flower dry weight were grouped together and contrasted with proportion of rhizome dry weight.

The results of factor analysis are presented graphically in Figures 4 to 9 (pages 90 to 92). In these figures each of the first four factors

Table 25: Key to plant characteristics in factor analysis

Number	Characteristic
1	Leaf area of largest leaf
2	Leaflet length
3	Leaflet width
4	Leaflet length-width ratio
5	Petiole length
6	Plant height
7	Plant width
8	Plant height-width ratio
9	Above ground dry weight
10	Vegetative above ground dry weight
11	Root dry weight
12	Total dry weight
13	Mean rhizome internode length
14	Mean number of nodes
15	Rhizome dry weight
16	Proportion rhizome dry weight
17	Number of rhizomes
18	Rhizome length
19	Number of daughter plants
20	Proportion above ground dry weight
21	Proportion vegetative above ground dry weight
22	Flower dry weight
23	Number of flowers
24	Proportion root dry weight
25	Proportion branching nodes on rhizomes

Grouping of Plant Characteristics by Factor Analysis

Figure 4 Factor 1 verses 2
Key to numbers, page 89

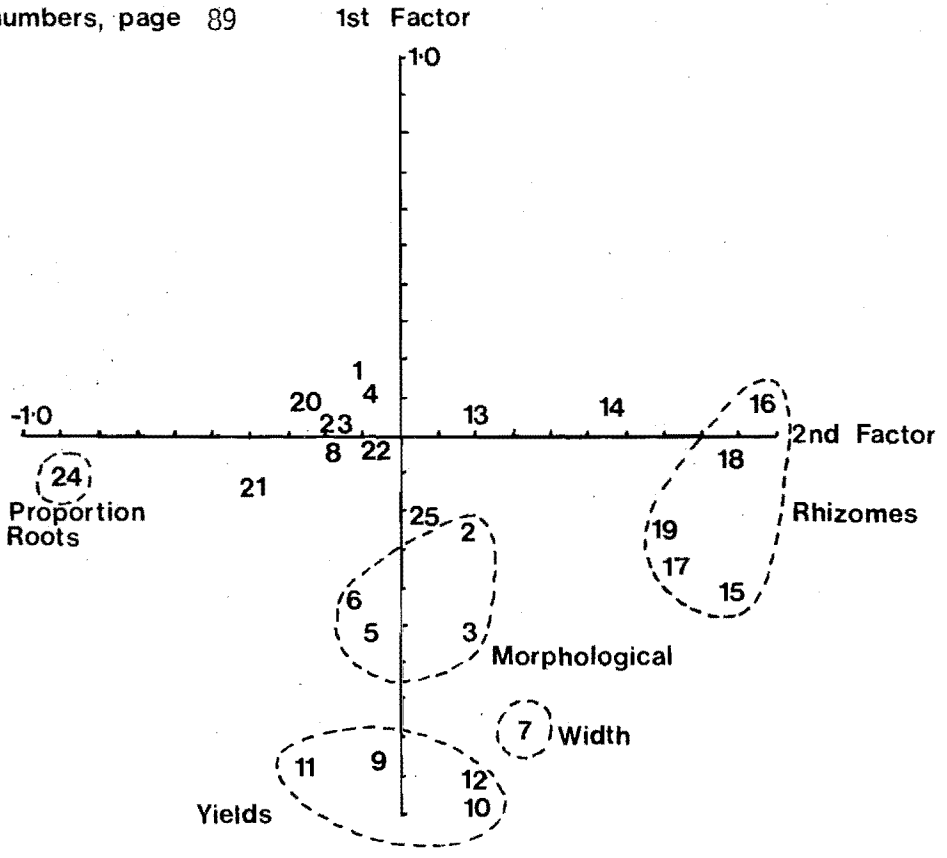
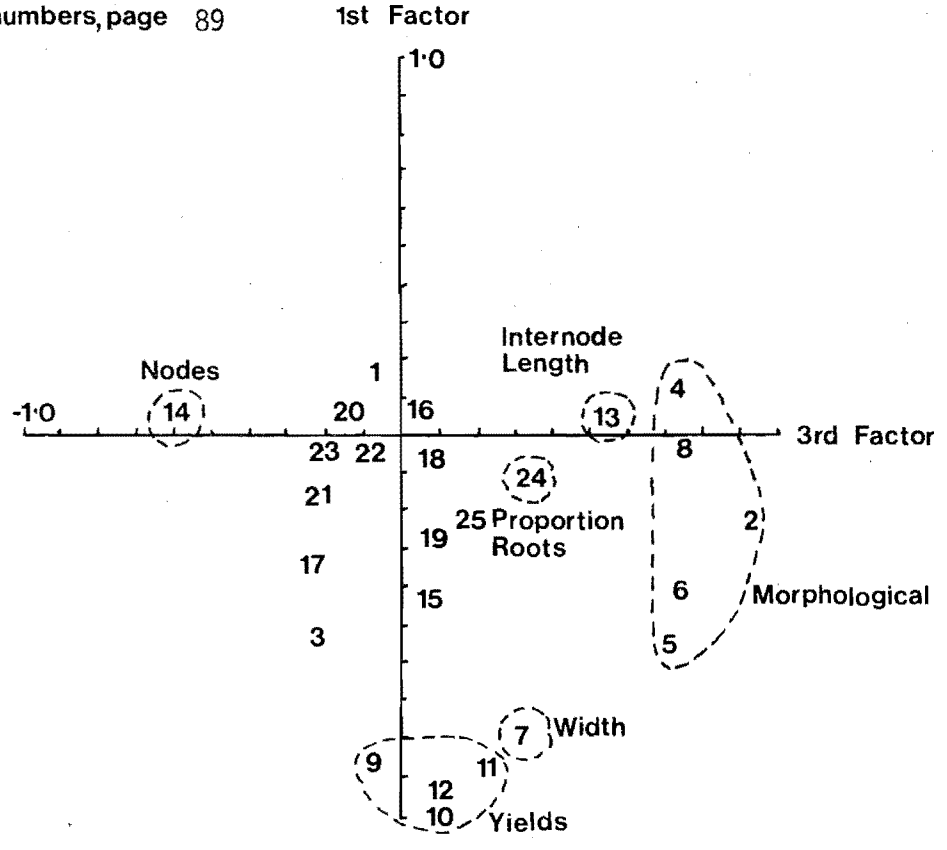


Figure 5 Factor 1 verses 3
Key to numbers, page 89



Grouping of Plant Characteristics by Factor Analysis

Figure 6 Factor 1 verses 4
Key to numbers, page 89

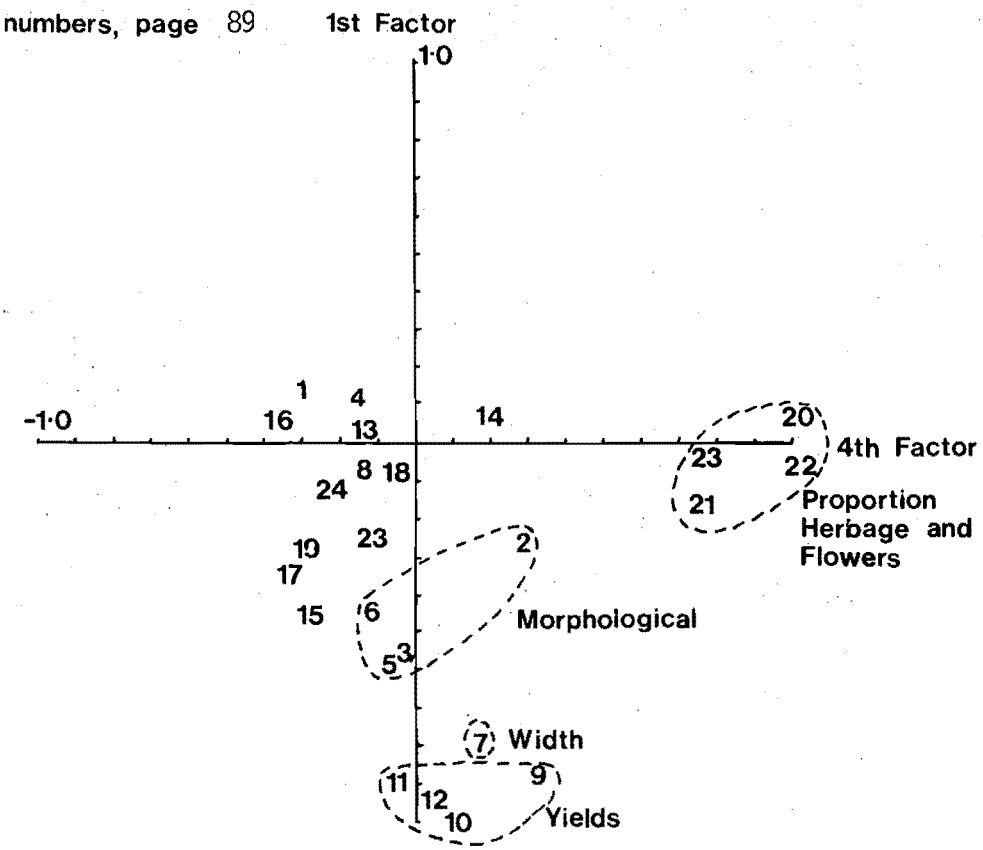
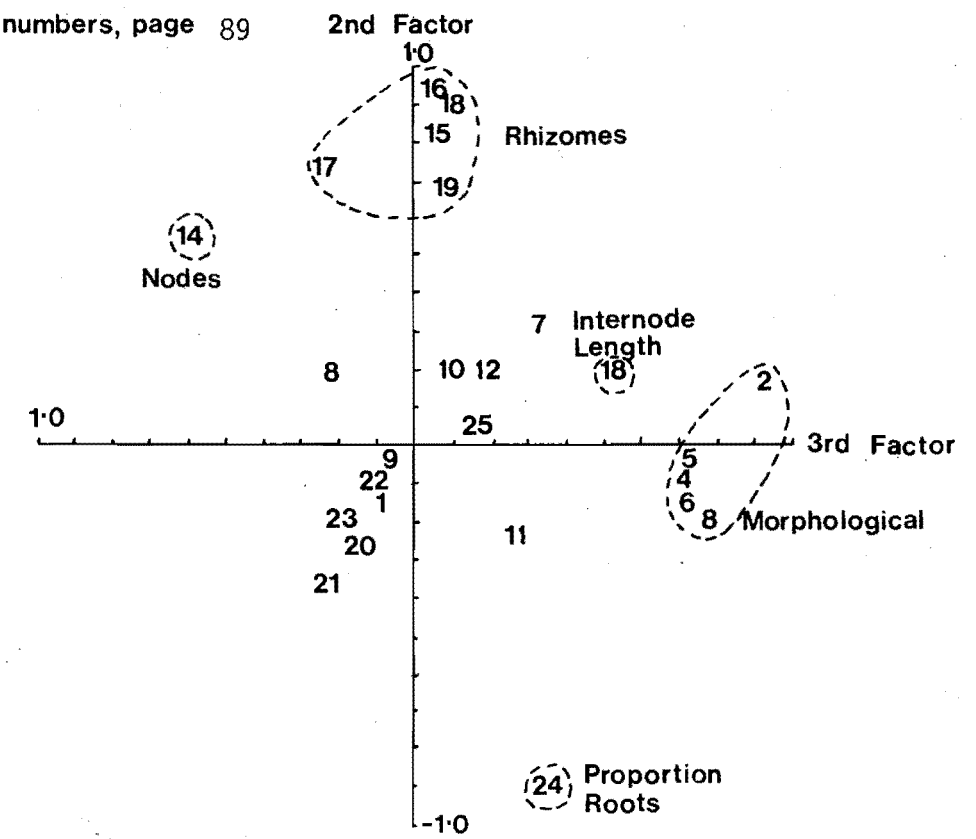


Figure 7 Factor 2 verses 3
Key to numbers, page 89



Grouping of Plant Characteristics by Factor Analysis

Figure 8 Factor 2 verses 4
Key to numbers, page 89

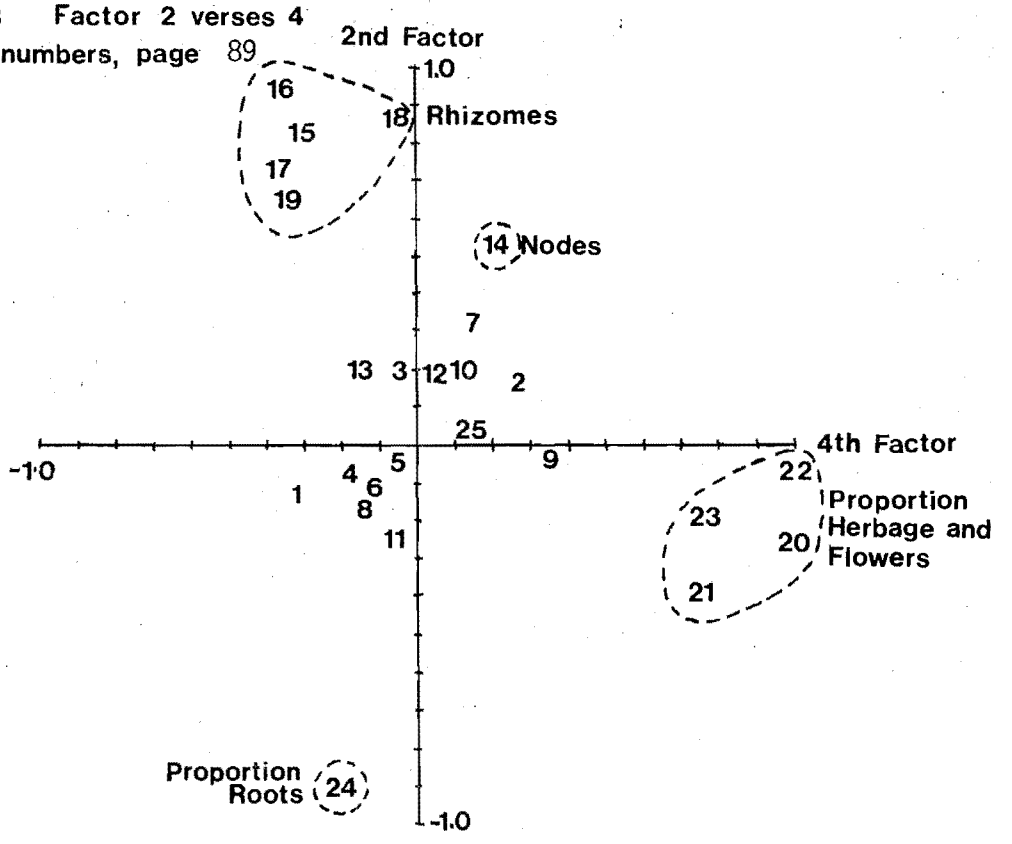
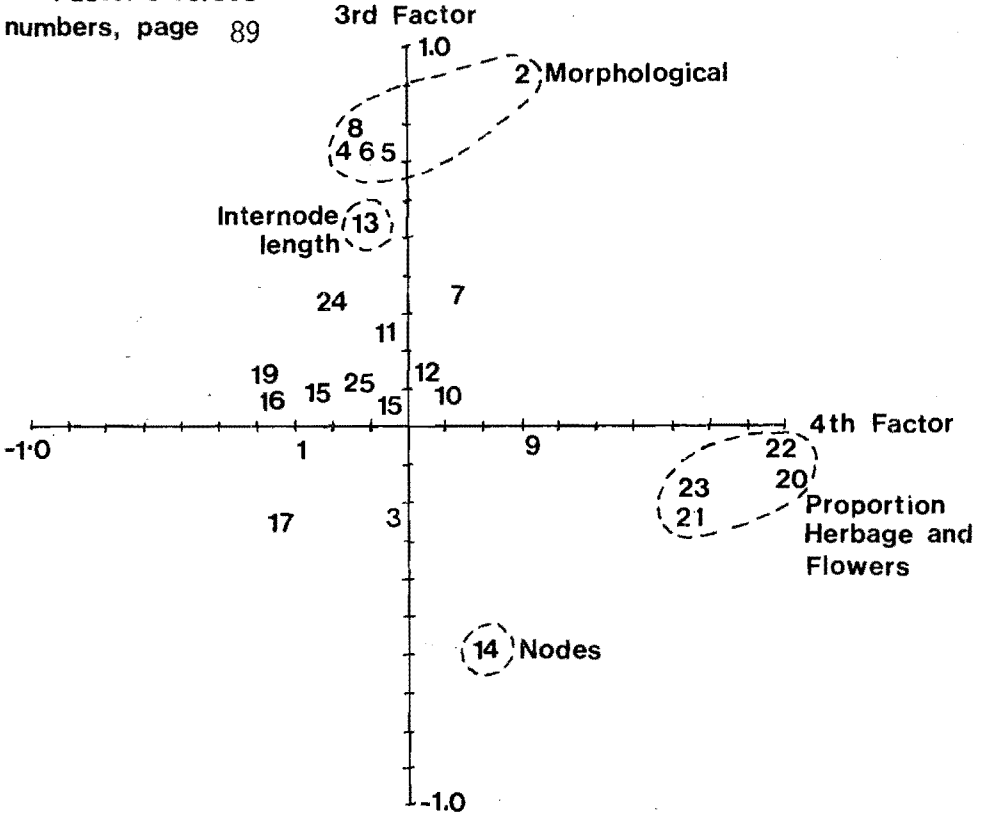


Figure 9 Factor 3 verses 4
Key to numbers, page 89



are graphed in turn against each of the other three. These figures resulted from the factor analysis table in Appendix D. On each of these figures, plant characteristics with factor values greater than approximately 0.3 were circled such that they fell into one of nine major groups.

The rhizome characteristics; dry weight, proportion consisting of rhizome dry weight, number of rhizomes, rhizome length and number of daughter plants consistently group together. This clearly depicts the high genotypic correlations between members of the group. The number of nodes on the longest rhizome tended to be near this group on most of the figures, indicating a low genotypic correlation, but was obviously not close enough to be included within the rhizome grouping. Mean internode length exhibited no consistent relationship with the rhizome grouping, but was negatively correlated with the number of nodes ($r_G = -0.56$). Mean internode length tended to be near the morphological grouping on some of the figures, indicating a low positive correlation with that group.

Rhizome branching had factor values consistently less than 0.3, and was therefore independent of all other measured plant attributes.

The morphological grouping tended to be very loose, it included the characteristics of leaflet length, leaflet width, leaflet length-width ratio, petiole length, plant height and height-width ratio. On some of the figures, leaflet length-width ratio and height-width ratio did not fall into this morphological grouping, indicating the independence of these two characteristics from the other morphological parameters. Leaf area was not related to any of the morphological characteristics, an unexpected result, as one would expect a positive correlation between leaflet length and leaf area. Most probably the variation in leaflet shape upset this expected correlation.

The attribute, plant width was consistently situated between the morphological grouping and the total, above ground and root dry weight grouping. Although plant width was expected to be a morphological characteristic the strong relationship with dry matter production would suggest otherwise.

Root, above ground, vegetative above ground and total dry weight were consistently grouped together, indicating a very high correlation between these characteristics.

The root dry weight proportion was not associated with any other characteristic, but it was consistently negatively correlated with the rhizome characteristics. This may suggest that highly rhizomatous plants have sacrificed roots rather than herbage to be rhizomatous. However, the lower proportion could just be a direct consequence of having a higher proportion of rhizomes.

Flower dry weight and the number of flowers were consistently grouped with the proportion above ground and the proportion of vegetative above ground dry weight. This may be the result of morphological changes attributable to flowering.

Genotype - Environment Interactions

Table 26 (page 95) presents the significances of genotype-environment interactions for all plant characteristics measured in more than one environment. Overall, the agronomic and production characteristics exhibited genotype-environment interactions while the morphological characters did not. It is also possible that some of the characters which showed no significant interaction did so for one of two reasons. The first was that the error variance was inflated. This could have been due to unforeseen variations within each experimental plot, by errors in measurement, and/or recording.

Table 26: Statistical significance of genotype-environment interactions for all measured plant characteristics

Significance Level		
<.01 probability	0.01 to 0.05 probability	not significant at 0.05
Proportion above gd. D.W.	Leaf width	Leaf area (2)
Vegetative D.W. (2)	Proportion root D.W.	Leaf F.W. (2)
Flower D.W. (2)	Rhizome length	Petiole F.W. (2)
Above ground D.W.	Number of daughter plants	Leaf length/width
Rhizome D.W.	Root D.W.	Plant height
Total D.W.	Proportion vegetative D.W.	Petiole length
Number of flowers		Height/width
Leaf length		Proportion flower D.W. (2)
Plant width		Proportion rhizome D.W.
		Number of rhizomes
		Number of nodes (2)
		Internode length (2)
		Rhizome branching (2)

2 - parameter measured for plants in only two environments

Secondly, the interaction term may have been low for characteristics measured in only two environments because the full range of environments was not represented.

In selecting for genetic improvement in *T. ambiguum* it would be desirable to use characteristics which exhibited low genotype-environment interaction to maximise selection responses and to produce cultivars adapted to a wide range of conditions,

The relevance of genotype-environment interaction is made clear in the following results of two contrasting selections made from cultivar Treeline.

Although Treeline had the highest yield of herbage at all sites it was not possible to distinguish any genotypes which were superior at all sites. Nevertheless, among the 27 Treeline genotypes used in the experiment seven were found to be higher-yielding than average for above ground dry weight, rhizome dry weight and total plant dry weight when grown at low altitude in Wakanui soil. At the high altitude site, five different genotypes were found to be better than average for the same three characteristics.

The seven genotypes selected from the lowland site were generally tall, erect and early flowering, while those selected as outstanding at the high altitude site were generally more prostrate, later flowering and highly rhizomatous.

Table 27 (page 97) presents the mean performance of the genotypes selected for the two environments. Genotypes which were superior in one environment were not necessarily superior in another, indicating that genotype-environment interaction was of major importance for these two

Table 27: Performance of two Treeline selections† relative to Treeline mean

Selection	Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
	Above ground dry weight				
low altitude	143*	144	140	105	92
high altitude	83	90	102	94	126*
	Rhizome dry weight				
low altitude	159*	103	192	106	99
high altitude	129	136	185	185	234*
	Total plant dry weight				
low altitude	136*	104	130	102	95
high altitude	86	104	110	109	148*

* environment from which genotypes were selected
† low altitude - seven genotypes
high altitude - five genotypes

selections. In general, the genotypes selected for the fertile lowland environment had below average performances in the infertile high altitude environment. Similarly, the genotypes selected for above average performance at the high altitude site had inferior performance, in terms of above ground and total plant dry weight, at the low altitude site. The rhizome dry weights of the high altitude selection were above average at all sites. This would indicate that highly rhizomatous genotypes had superior survival and production potential under harsh sub-alpine conditions.

The performance of the selections in the other three environments was generally intermediate between the two extreme environments. However, it is particularly noticeable that the low altitude selection also performs extremely well in the Wakanui soil at medium elevation. This would indicate that this selection was selected more on ability to respond to soil fertility rather than adaptation to climatic conditions at the low altitude site. The high altitude selection did not exhibit any marked superiority in infertile soils, the Cass soil at other locations, and it is likely that this selection was selected on adaptability to the harsh climatic conditions.

It is therefore apparent that there was differential selection pressures acting on *T. ambiguum* in this range of environments. In fertile soils, the selection pressure favoured genotypes with the ability to be very productive under fertile conditions. At the high altitude site the selection pressure was for genotypes which could survive the harsh climatic and edaphic conditions.

4.2 EXPERIMENT TWO

Herbage Production

The mean dry matter yields for each treatment are given in Table 28 (page 99). From this table it can be seen that all irrigation responses

Table 28: Mean dry matter yields (gm^{-2}) of an established stand of c.v. Treeline

Height frequency	Ground Level monthly	8cm monthly	Ground Level 2 monthly	8cm 2 monthly	Ground Level at Flowering	8cm at flowering
27/ 9/77	199.9 a	98.7 b				
18/10/77	140.8 c	128.0 c	461.0 a	266.3 b		
17/11/77	145.0 c	124.4 c			608.2 a	336.8 b
13/12/77	119.0 c	60.4 d	342.1 a	208.8 b		
11/ 1/78	45.5 a	28.1 b				
13/ 2/78 (Irrigation)	83.6 b (238.4) a	0.0 c (98.6) b	114.6 b (203.3) a	0.0 c (132.4) b		
15/ 3/78 (Irrigation)	62.3 b (135.2) a	39.4 c (76.6) b				
12/ 4/78 (Irrigation)	59.7 c	65.7 c	148.8 a (172.7) a	85.3 b (129.6) b		
6/ 6/78	78.4 b	60.0 c	145.6 a	77.7 b		
Total	934.2 d (1161.9) c	604.7 g (740.5) f	1212.1 b (1324.7) a	638.1 g (814.8) e	608.2 g	336.8 h

At any date, treatments with some letters are not significantly different using Duncan's new multiple-range test at 0.05 probability.

Each mean is from an $18m^2$ area.

were significant except the April 2-monthly cut. Cutting to ground level yielded significantly more than cutting to 8 cm except for three of the monthly cuts. However, this would be expected because of the low position of growing points in this low crowned clover.

The best seasonal yield was equivalent to 13250 kg ha^{-1} and was obtained by cutting irrigated plots to ground level every two months. Without irrigation the same cutting treatment indicated a yield equivalent to 12100 kg ha^{-1}.

The monthly cut was not taken in May because the sward had produced negligible herbage since April. However, the subsequent harvest in June revealed that, although neither treatment had been cut for two months, the plots previously cut every two months yielded significantly more than those cut every month. This is an indication that the monthly cuts never completely recovered before cutting again, resulting in depletion of plant reserves.

Growth Rates

The growth rates of the monthly and 2-monthly cuts to ground level are given in Figure 10 (page 101). From this figure it can be seen that the growth rates in spring were significantly higher than those attained later in the season. The 2-monthly cuts had significantly higher growth rates in their second month of growth than their first until January when water stress depressed herbage production.

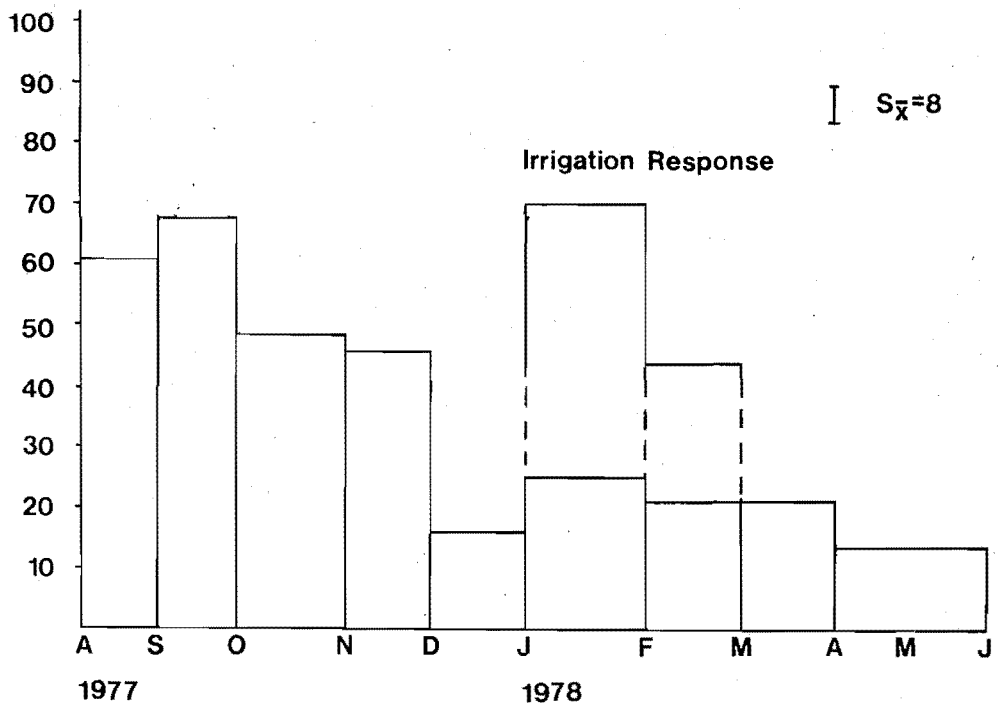
Flowering Scores

The mean flowering scores for each treatment are presented in Table 29 (page 102).

The assessment indicated that cutting suppressed flowering in the following month. It is also clear that cutting to ground level had a greater

Figure 10: Mean growth rates (kg ha^{-1} day^{-1}) of cv Treeline

a. Cut monthly to ground level



b. Cut two monthly to ground level

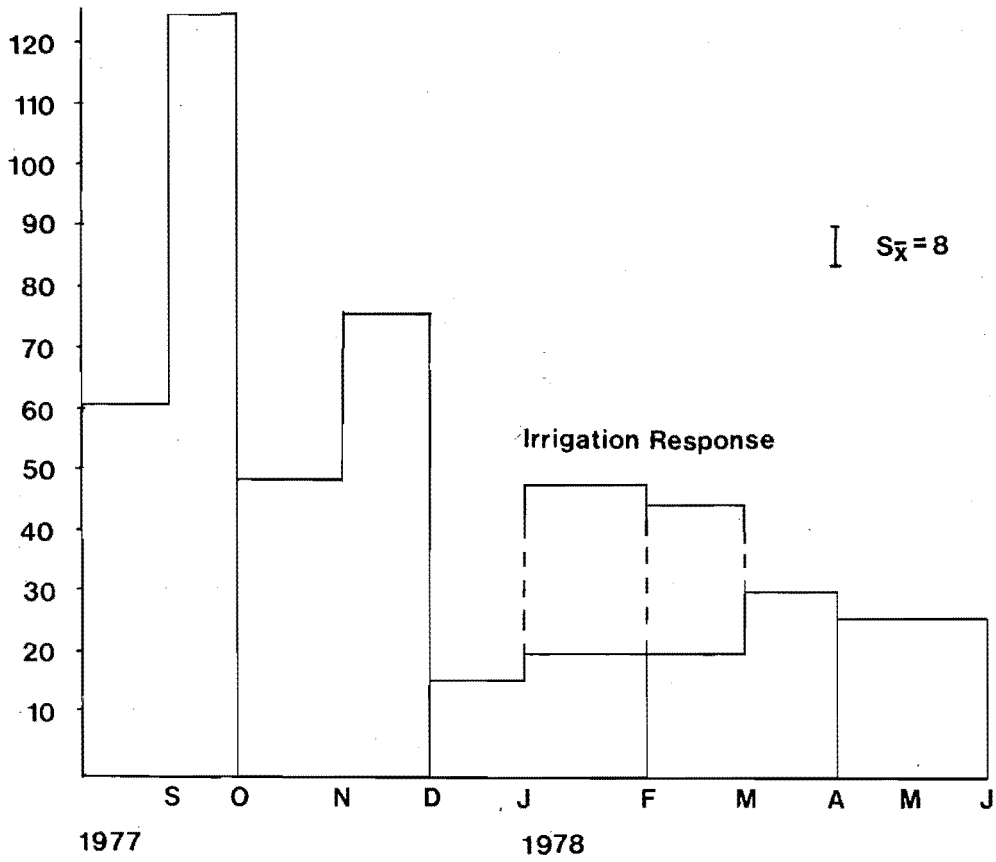


Table 29: Flowering scores for November and December, Mean of each treatment

Treatment		Month	
Height	Frequency	November	December
ground	monthly	*0.8 d	*0.1 e
8 cm	monthly	*2.4 c	*0.8 d
ground	2 monthly	*0.4 d	3.7 c
8 cm	2 monthly	*1.0 d	5.3 b
ground	flowering	4.1 b	*0.1 e
8 cm	flowering	4.6 ab	*0.6 de
control	control	5.3 a	8.5 a

* cut previous month

Within any month, treatments with the same letter beside are not significantly different using Duncan's new multiple-range test at 0.95 probability

effect than cutting to 8 cm.

Seed Yields

The seed yield of two 1 m^2 samples taken from the border area were 69.7 gm^{-2} and 50.3 gm^{-2} respectively.

Root and Rhizome Yields

The dry matter yields of root and rhizome from the 0.5 m^2 sample taken from the border area was 1164 gm^{-2} in the top 17 cm, 80 gm^{-2} between 17-35 cm and 19 gm^{-2} below 35 cm to a depth of 80 cm. Below 80 cm there were no roots greater than 2 mm in diameter. It is possible, however, that some of these could have continued for another 30-35 cm. The total root and rhizome mass was therefore equivalent to 12600 kg ha^{-1}, which is comparable to the total seasonal herbage production for the highest yielding treatments.

Weed Ingress

Although visual scoring of weed ingress did not show any differences between treatments, it was apparent that towards the end of the experiment white clover was present in most plots. It also tended to be more vigorous in plots which were cut to ground level every month, where the treatment tended to be unfavourable for *T. ambiguum*.

Plate 6(a). Treeline Production Trial

The site in January 1978 showing dense mass of flowerheads typical of samples producing 500 - 700 kg ha^{-1} of seed. Also green regrowth of previously cut plots.

Plate 6(b).

The site in February 1978 showing irrigation response in foreground.

CHAPTER 5

DISCUSSION

This discussion seeks to clarify all major aspects of the complex set of results obtained in experiment one. When appropriate, the results of experiment two are related to these.

Firstly the effect of varying plant vigour at transplanting is discussed in relation to the results obtained. The discussion then leads into genetic differences observed and to aspects of morphological, floral and rhizome characteristics, herbage production and the relationships among them. Environmental effects are discussed next, followed by a short section discussing the importance of genotype-environment interactions. This is then followed by sections on selection potential, criticism of techniques and suggestions for future research. Lastly the concluding summary is an attempt to tie together and summarise all major aspects of the research.

5.1 OBSERVATIONS AT TRANSPLANTING

At the time of transplanting Prairie had less root growth than the other *T. ambiguum* varieties, while Forest and Summit had less top growth. These differences showed up later in the experiment as a lower proportion of root dry matter for Prairie and lower total plant dry weights for Forest and Summit. Whether or not the poor growth at transplanting lead to the final results or whether both measurements reflect the same genetically -, determined characteristic, is unknown. They probably both reflect the same characteristic, that of low root 'vigour' in Prairie and low overall 'vigour' in the diploids, Forest and Summit.

5.2 MORPHOLOGICAL CHARACTERISTICS

The four polyploid varieties, Prairie, C.P.I. 57353, Treeline and C.P.I. 51140 had longer leaflets than the two diploid varieties, Forest and Summit, under all conditions. Similarly, the area of the largest leaf was greater in the polyploids. Although mean area per leaf showed a consistent increase with ploidy, leaflet length did not.

Cultivar Prairie had shorter leaflets and lower leaf areas than was expected from observations of the well established parent plants in the field, some of which had leaflets over 8 cm in length. Similarly, in the Register of Australian herbage plant cultivars (1977) Prairie is described as having leaflets twice as long as Summit, Forest and Treeline under good growing conditions. As the experimental site on Wakanui soil at Lincoln College was adjacent to the large leaved parent plants, it is assumed that the leaves were smaller than expected because the plants had only been established for one season and were still too immature to produce the extra large leaves. However, the other varieties did not appear to be affected in this way.

Results for leaflet length and leaf area were in general agreement with those of Kannenberg and Elliott (1962) and Baysal (1974). They too found that mean leaf area and leaflet length tended to increase with ploidy, although there existed a large amount of overlap between ploidy levels.

The correlation between leaflet length and leaf area was not significant, probably because of varying leaflet shapes. For example, the mean leaflet length-width ratio for the varieties varied from 1.34 in Forest to 2.61 in C.P.I. 51140. Both hexaploid lines had mean leaflet length-width ratios lower than that of C.P.I. 51140, but one of the hexaploid lines, C.P.I. 57353 had a higher ratio than the tetraploid cultivar, Treeline. These results were

similar to those obtained by Kannenberg and Elliott (1962), who found that the tetraploids had a higher mean ratio than the hexaploids under field conditions while the diploids had the lowest ratios. Baysal (1974) reported that, although some tetraploid plants had very high ratios, the means of the tetraploids and hexaploids were quite similar. As these researchers used different plant populations to those used in the present experiment minor differences would be expected.

The values given for mean leaflet length-width ratio by Barnard (1972) and the Register of Australian herbage plant cultivars (1977) for cvv. Summit, Forest, Treeline and Prairie of 1.34, 1.50, 1.76 and 1.50 respectively are similar to the mean values over all environments of 1.38, 1.34, 1.80 and 1.60 obtained in the present experiment. Forest was perhaps lower than expected, however, as the sample size of Australian results were not mentioned it is possible that their quoted value was unrealistically high. As the mean leaflet length-width ratio was very stable throughout the several environments, with no more than a 16 percent change, the similarity with the Australian results was to be expected.

The two components of leaflet length-width ratio (leaflet length and leaflet width), had heritabilities of 57 percent and 46 percent respectively, indicating a high degree of genetic control. Although these two components were genetically independent (r_G = 0.07), the similarity of response to environmental conditions would have caused leaflet length-width ratio to have an even higher heritability of 68 percent, the highest for any characteristic measured in the experiment.

Leaf characteristics generally exhibited less genetic variation within each variety than other plant characteristics. In general, their genotypic

coefficients of variation (GCV) were only 10 to 20 percent while other characteristics ranged from 20 to over 70 percent.

Under favourable conditions, Treeline and C.P.I. 57353 had the longest petioles while the diploids had the shortest. It seemed, however, that under relatively harsh environmental conditions potential differences in petiole length were unable to be expressed. Despite a high correlation (r_G = 0.88) between petiole length and plant height, varieties which had the longest petioles were not necessarily the tallest. Cultivar Treeline and C.P.I. 51140, the two tetraploid lines, were the tallest while the two diploid lines, Forest and Summit, were the shortest. The two hexaploid lines, C.P.I. 57353 and cultivar Prairie, tended to be intermediate in height. This was in contrast to Baysal (1974) who found tetraploids to be the shortest. Considering that some of the plants he used were collected from the same region as C.P.I. 51140, namely Eastern Turkey, and that he included the parent line of cultivar Summit, C.P.I. 2264, the results were unexpected. However, as the mean height of his tetraploids was 9.3 cm, similar to C.P.I. 51140 in good conditions, it is likely that the different diploid and hexaploid populations used would account for these differences.

Generally, tall varieties were more erect than shorter ones. There were, however, erect plants within most populations, a result similar to that found by Kannenberg and Elliott (1962), Townsend (1970) and Baysal (1974). In the present experiment, the populations with the highest mean plant height-width ratio, an index of growth habit, were both tetraploid. The other two ploidy levels were generally more prostrate.

The genetic variation within each variety for both petiole length and plant height was generally greater than for leaf characteristics,

Similarly, the heritabilities at 47 percent and 35 percent for plant height and petiole length respectively were lower than for leaf characteristics. However, because of the large genetic variability and relatively high heritability, selection of tall or short plants should be relatively easy, provided, of course, that the narrow sense heritability was also relatively high.

The percentage of plants within Summit which had leaf markings, 60 percent, was slightly lower than the 85 percent reported by Barnard (1972). However, considering that the sample size in the present experiment was only 30 these two percentages may not be significantly different. Within cultivar Treeline the percentage of leaf marked plants was 60 percent compared with Barnard's (1972) report of 18 percent. Even considering the small sample size the result obtained was higher than expected. As plants in the present experiment were established from clones of first generation seed of Treeline it is possible that Barnard's (1972) estimate was unrealistically low.

Huia white clover had smaller rounder leaflets than any of the *T. ambiguum* varieties. Similarly, Maku had leaves of about the same length as Huia, but were generally narrower. The petiole length of Huia was similar to Treeline under all conditions, while of course, Maku has no petioles. However, despite the similarity of petiole lengths, Huia plants were generally shorter than Treeline plants under all conditions. Huia was, as one would expect, very prostrate because of its stoloniferous growth habit. Maku was exceptionally tall and erect under good growing condition but similar to Treeline in poor conditions. This was most likely due to changes in the growth morphology of Maku during flowering. Under poor conditions flowering

had not occurred at the time of measurement so there were no morphological changes.

A low frequency of multiple leaflets (leaves with more than three leaflets) was observed to occur predominantly on daughter plants of 40 percent of Treeline genotypes. These were observed on plants at all locations, including the second experiment. Why this phenomenon occurred predominantly on daughter plants is unknown. Physiological studies may reveal that it is related to levels of growth substances in the rhizomes during leaf formation.

From the results of factor analysis it appears that characteristics for greater plant size tend to be inherited together in a similar manner to that which Davies and Young (1967) found in white clover *(T. repens)*. These researchers found that large-leaved plants had longer petioles, were heavier and spread more. Since then Caradus (1977) has found that large-leaved white clover lines, the 'Ladino' types, also tend to be more taprooted than the smaller leaved types, which tend to have very fibrous root systems. In *T. ambiguum*, genotypes with high total, root and above ground dry weights also tended to be taller, wider, with longer petioles and wider leaflets. There was also a slight tendency towards higher rhizome dry weights but the other rhizome characteristics were independent. Growth habit, flowering date and leaflet shape were also independent of the size characteristics, similar to that which Davies and Young (1967) found in white clover.

5.3 FLOWERING AND SEED PRODUCTION

The mean flowering dates for each variety at each site were difficult to determine accurately because of the large variation in flowering date within each variety. Also, all plants did not flower at some of the harsher sites biasing the estimates of mean flowering date. However, both varieties

within each ploidy level behaved similarly. It was clear that the diploids tended to be the earliest flowering followed by the tetraploids and lastly, the hexaploids. These results were similar to those obtained by Kannenberg and Elliott (1962). Reinforcing the view that flowering became later with increasing ploidy was the observation that cumulative flowering percentages decreased with increasing ploidy under all environmental conditions. In contrast to this, Baysal (1974) found that at the time when 72 percent of the diploids had flowered 84 and 67 percent of the tetraploids and hexaploids had flowered respectively. This indicates that in his experiment the tetraploids flowered earliest. Under the most favourable conditions in the present experiment, the Wakanui soil at low altitude, when 70 percent of the diploid plants had flowered, approximately 60 and 15 percent of the tetraploids and hexaploids had flowered respectively. These differences, between the present work and Baysal's (1974), are most likely accounted for by the use of different plant populations.

In contrast to Kannenberg and Elliott (1962) and Baysal (1974), the mean number of flowerheads per flowering plant did not increase with ploidy level. In fact the only significant difference was that the diploid line, Summit had significantly more flowerheads than the later flowering hexaploid, 57353, at one of the sites. This was most likely attributable to earlier flowering of Summit allowing more flowerheads to be produced before harvest in March. However, under favourable conditions of the Wakanui soil at low altitude the maximum number of flowerheads produced was found to increase with ploidy level. These increased from 101 to 163 to 176 in the three ploidy levels respectively (Appendix B).

Treeline was found to have the smallest flowerheads, a result which was in agreement with Barnard (1972), who reported that Treeline had relatively small flowerheads.

In general, Huia initiated flowering about one month earlier than the diploid *T. ambiguum* varieties at all sites. Maku Lotus, on the other hand, began flowering one and a half months later than Huia at all sites.

The present study, with similar photoperiod conditions at each location, showed clearly that day length requirements were not the major factor determining floral initiation. It was possible, however, that plants were too small and immature to flower when day lengths were conducive to flowering and could only flower when mature enough to do so. It as also possible that temperature played a major role in initiating flowering. In the Cass and Bealey soils there was a correlation of $r = 0.89^{**}$ between mean monthly temperature and cumulative flowering percentage. However, this does not mean that temperature was the 'triggering' mechanism. Most likely, flowering was related to plant size or maturity and this was related to temperature. This would also account for the earlier flowering in the more fertile Wakanui soil and the relatively low heritability (31.9%), indicative of large variability within genotypes which was typical of plant size and dry matter yields.

Seed yields of Treeline in experiment two were found to reach levels equivalent to 500 to 700 kg ha^{-1}. Although commercial yields would be lower than this because of the inevitable losses it is an indication that seed yields of Treeline are adequate. These figures for seed production compare favourably with seed yields of other legumes, such as white clover, red clover and lucerne under Canterbury conditions (Smetham pers. comm.).

5.4 RHIZOME CHARACTERISTICS

Under all the environmental conditions Prairie and Treeline produced the greatest mean rhizome dry weight while Summit produced the least. The other three varieties, 57353, 51140 and Forest were intermediate at all the experimental sites. Although Prairie and Treeline produced similar dry weights the proportion of their total dry weight which consisted of rhizome dry weight differed. The mean proportion of rhizome dry weight in Prairie was 30 percent while that of Treeline was 22 percent. Summit was the lowest with 8 percent while Forest, 51140 and 57353 had 21, 18 and 17 percent rhizome dry weight respectively.

These varietial differences were predominantly due to differences in the number of rhizomes, rhizome length and the proportion of plants within each variety which produced rhizomes. To a lesser extent some of the varietal differences were due to branching of the rhizome system.

As the number of rhizomes per plant was highly correlated with rhizome dry weight (r_G = 0.85) and with the proportion of rhizome dry weight (r_G = 0.78) it was expected to find that Prairie and Treeline had the most rhizomes while Summit had the least.

In contrast to Kannanberg and Elliott (1962) and Baysal (1974) the number of rhizomes did not show any consistent increase with increasing ploidy. However, the results for Summit and 51140 were in agreement with Baysal (1974) who found that the parent line of Summit, C.P.I. 2264 had fewer rhizomes than tetraploid genotypes collected from the same region as C.P.I. 51140.

As there were consistently more Summit and 57353 plants without

rhizomes than Prairie at each site this would be part of the reason why these two varieties exhibited a lower mean rhizome dry weight. These effects would be greater in harsh environments where the proportion of plants producing rhizomes within each variety ranged from 60 to 95 percent.

Although rhizome length was correlated with rhizome dry weight (r_G = 0.74) and proportion of rhizome dry weight (r_G = 0.84) variety means for rhizome length did not exhibit the same trends as these two characteristics. Under favourable climatic conditions in a relatively unrestrictive soil, friable with low bulk density, rhizome length was found to increase with increasing ploidy. In restrictive edaphic conditions, a compact soil of high bulk density, or under harsh climatic conditions the potential differences were unable to be expressed.

The results for rhizome length were in general agreement with both Kannenberg and Elliott (1962) and Baysal (1974) who found that rhizome length increased with increasing ploidy level.

Of the two components of rhizome length - mean internode length and number of nodes - only mean internode length was found to increase with increasing ploidy level under unrestrictive edaphic conditions. The number of nodes also exhibited a ploidy level effect, but for this parameter diploids had the most and tetraploids had the least. The hexaploids had an intermediate number of nodes. Under restrictive edaphic conditions these effects were not apparent.

The low proportion of branching in the rhizome systems of Summit and 57353 probably partially accounts for the lower rhizome dry weights of these two varieties. Similarly, the high proportion of branching in Treeline's

rhizome system probably accounts for part of the reason why this variety produced a high rhizome dry matter. However, as the correlation between branching and rhizome dry weight was relatively low (r_G = 0.18) the effect of branching on rhizome dry matter was probably minimal. This effect may, however, increase in importance as the branches increase in size in subsequent years.

The number of daughter plants was more highly correlated with the number of rhizomes (r_G = 0.85) than rhizome length (r_G = 0.55) or the proportion of rhizome branching (R_G = 0.18). This, along with the results of factor analysis, where daughter plant number and rhizome number had similar values for each factor, indicate that the number of daughter plants was controlled more by the number of rhizomes than the other two factors. However, it would be quite likely that the proportion of rhizome branching contributes more to daughter plant numbers in subsequent years after the branches have had a chance to grow to the surface. Because of the correlation with rhizome number it was not unexpected that Prairie and Treeline had more daughter plants than Summit while the other three varieties were intermediate.

In contrast to Kannenberg and Elliott (1962) and Baysal (1974) the number of daughter plants did not show any consistent increase with increasing ploidy level. Once again, this difference was probably a reflection of the different populations studied.

Although the nutritional status of the Cass soil, and consequently the plants total dry matter production, was poorer than on the Wakanui soil rhizome development was less restricted. This was because of the lower bulk density of the Cass soil (0.7) compared with the Wakanui soil (1.5). At the

medium altitude location rhizome length was found to be 75 percent longer in the Cass soil than the Wakanui soil. The increase in rhizome length was predominantly attributable to a 55 percent increase in mean internode length while the number of nodes only increased 16 percent. The proportion of branching rhizomes was found to be lower in the Cass soil than the Wakanui soil. The better nutritional status of the Wakanui soil, as reflected in the total plant dry matters, probably caused a partial loss of apical dominance in the rhizome system. As McIntyre (1972) has shown that nitrogen was the major factor associated with apical dominance in the rhizomes of *Agropyron repens* it is possible that nitrogen is of similar importance in *T. ambiguum*. If this is true, there may be a tendency for effectively nodulated plants to produce more branching rhizomes. As effectively nodulated plants should also be more vigorous, one would expect a positive correlation between total plant dry weight and rhizome branching. Although both the phenotypic (r_P = 0.28) and the genotypic correlation (r_G = 0.27) were positive they were not very high. Similarly as weight per rhizome per unit length is highly correlated with rhizome branching (R_G = 0.63) it could be considered as an alternative measurement of rhizome branching. It was also positively correlated (r_P = 0.28 and r_G = 0.38) with total plant dry weight. Even though the above correlations are not very high they are indicative that effectively nodulated plants tend to produce more branching rhizomes.

The broad sense heritabilities for rhizome dry weight, proportion rhizome dry weight, rhizome length and number of rhizomes were between 28 and 29 percent while that of daughter plant number was only 11 percent. This is in contrast to heritabilities calculated from Baysal's (1974) work of 69 percent for plant spread and 88 percent for daughter plant number in the field. The heritabilities calculated for the experiment were probably

lower than Baysal's because of the use of five very diverse environments, genotype-environment interaction and having only two replicates. Baysal (1974) had only one environment with four replicates. The heritability estimate of daughter plant number is probably low in the present experiment because of the high number of plants which did not produce any daughter plants. In Baysal's experiment the mean number of daughter plants produced was much higher between 10 and 30 whereas the maximum variety mean, in the present experiment, was only 10.

The number of nodes had a heritability of 24 percent while internode length had a higher heritability of 40 percent, an average value for the morphological characteristics. The degree of branching of the rhizome system had a heritability of 17 percent while weight per rhizome per length, an alternative indication of branching, had a heritability of 32 percent.

In general, the genetic variation within each variety for rhizome characteristics was high, with genotypic coefficients of variation between 30 and 50 percent. However, Summit was generally less variable with genotypic coefficients of variation below 26 percent. Treeline was particularly variable for rhizome dry weight (GCV% = 80) and number of rhizomes (GCV% = 59). With these high genotypic coefficients of variation and average heritabilities, for this experiment, the potential for selection of rhizome characteristics is extremely good. Also, because of their high correlation with daughter plant number, selection based on this may offer a simple parameter for selection, even though the heritability of daughter plant number was low.

In experiment two the underground dry weight of a pure stand of cultivar Treeline was found to be equivalent to 12600 kg ha^{-1}. The majority

of this consisted of rhizomes above 17 cm. This mass of rhizomes must be able to act as a huge reserve of assimilates and energy. The high rate of spring growth may only be possible by drawing off these assimilates.

5.5 HERBAGE PRODUCTION

Kannenberg and Elliott (1962) found that in a wide range of lines tested C.P.I. 10803, the parent line of Prairie, and C.P.I. 2264, the parent line of Summit were the highest and least productive respectively. As these two varieties were included in experiment one it is probable that most of the agronomic variation within *T. ambiguum* was studied.

The genetic variation within each variety for above ground dry matter was high, with the genotypic coefficients of variation between 40 and 60 percent. Because of the large variation within each variety there was a large amount of overlap between varieties. However, in spite of this variation Treeline generally produced the most above ground dry weight. Apart from 57353 producing a similar amount to Treeline in the Wakanui soil at Lincoln College the hexaploids generally produced 15 to 30 percent less at all sites. Similarly, 51140 generally produced 30 to 40 percent less at all sites. Under the relatively favourable climatic conditions at Lincoln College the diploids produced 30 to 50 percent less than Treeline. However, at the medium elevation at Cave stream they produced nearly as much herbage as Treeline. This may be due to superior drought tolerance of the diploids (Bryant, 1974). At the high altitude site the diploids produced 15 to 30 percent less than Treeline.

Little importance can be attached to the herbage production figures as nodulation was not studied. Therefore, yields may reflect nodulation efficiency and/or adaptation to the environmental conditions. This is of

course, a problem when dealing with legumes, their genetic performance can quite easily be limited by inefficient *Rhizobium* strains or by an inherently poor nodulation ability of the plant genotype. Only by testing in a rhizobia free situation with controlled amounts of nitrogen would it be possible to distinguish inherently 'vigorous' genotypes. It would have been ideal if such an environment could have been included in the experiment. However, the experiment still provided useful information on herbage production for plants grown in the presence of the rhizobia cultures applied. It is not possible, however, to extrapolate these results for performances under different rhizobial conditions.

The above ground dry matter production of the *T. ambiguum* varieties was only 15 to 20 percent of Huia under favourable environmental conditions. As the environment became harsher *T. ambiguum* performed relatively better compared with Huia. At the high altitude site Treeline produced 37 percent as much as Huia. However, as the best plants of *T. ambiguum* generally produced two to three times as much as the Treeline mean the above ground dry matter production of these plants exceeded Huia at the high altitude site.

Under good conditions Huia produced more than Maku while under the harsh high altitude conditions they were not significantly different.

Because *T. ambiguum* had a large proportion below ground the total plant dry weights of Treeline at the harsh high altitude environment was slightly greater than Huia. However, in favourable conditions Huia and Maku still had a greater total plant dry weight than any of the *T. ambiguum* varieties. As the best *T. ambiguum* plants at each site consistently had total plant dry weights 2 to 2.5 times greater than the Treeline mean

(Appendix B) they also had total plant dry weights greater than Huia and Maku.

The broad sense heritability estimates for vegetative above ground dry weight was 31 percent, a figure which was medium for this experiment. The proportion above ground dry weight had a heritability of 24 percent. The heritability of above ground dry weight was only 16 percent and was probably low because of the inclusion of flower dry weight, a parameter very susceptible to environmental influences. These estimates of heritability, along with the estimates of genotype coefficient of variation, which were around 30 to 40 percent, are indicative of reasonable selection responses for herbage or total plant yields.

The first factor of factor analysis grouped together total, herbage and root dry weight and showed that as these characteristics increased plant height, width, petiole length, leaflet width and rhizome dry weight all tended to increase. This shows that higher producing genotypes were taller, wider and had larger leaflets, they also had a tendency to produce more rhizomes.

In experiment two Treeline produced equivalent to 13250 kg ha^{-1} in an irrigated pure stand cut every two months. The same cutting treatment without irrigation still produced 12100 kg ha^{-1}. This high production without irrigation was because most of the growth was in spring before the dry period, when there was little growth without irrigation. When cut every month the sward produced 11600 kg ha^{-1} with irrigation and 9300 kg ha^{-1} without. Cutting every month had the effect of reducing plant reserves, such that by the following autumn the rate of regrowth was slower, 14 kg ha^{-1} day^{-1} compared with 26 kg ha^{-1} day^{-1} for the plots cut two-monthly. Cutting to

8 cm was wasteful as the growing point of *T. ambiguum* is near the ground. The 8 cm of petiole left subsequently decays, it may, however, act as a mulch, conserving water.

The herbage production, although not compared directly with other legumes, compares favourably with the annual figure of 14200 kg ha^{-1} produced by a stand of 'Pawera' red clover in a Wakanui Silt Loam under Canterbury conditons (Vartha and Clifford, 1978). The yield of *T. ambiguum* exceeded that of white clover 'Huia' and 'Pitau', producing over 3000 kg ha^{-1} more. Whether *T. ambiguum* could sustain this yield in subsequent seasons remains to be seen. It is possible that the herbage production under cutting was drawing off reserves of the massive rhizome system. Therefore the weakened sward might be less productive in subsequent years.

5.6 ENVIRONMENTAL EFFECTS

The environmental effect can be partitioned into two components, effects caused by soil differences and those due to the climatic differences at the three altitudinal sites.

5.6.1 SOIL

The three soils used in the experiment were both chemically and physically very different. The Wakanui Silt Loam, occurring naturally at the low altitude site, contained high levels of most of the major plant nutrients (Appendix A) and organic matter. It was, however, very compact with a high bulk density (1.5 - 1.6). In contrast to this, the Cass soil, occurring naturally at the medium elevation site, had low levels of most of the major plant nutrients and organic matter. Even after a dressing of 50 kg ha^{-1} of phosphate and other nutrients was applied the nutrient status of this soil was still much lower than the Wakanui Silt Loam. In spite of

this, bulk density of the Cass soil was very low (0.7), typical of high country soils subject to frost heave. The Bealey soil, occurring naturally at the high altitude site, had a slightly lower nutrient status than the Cass soil but a similar bulk density (Appendix A).

Soil water deficits would have been absent at the low altitude site where regular watering was carried out. At the medium elevation site, however, the soil water deficit could have become an important factor limiting plant growth, especially during February when only 8.6 mm of rain fell. At the high altitude site it was unlikely that soil water deficit became a critical factor limiting plant growth as it is only rarely that a soil water deficit occurs in this region, at altitudes greater than 1000 m (McCracken pers. comm.). Although summer rainfall is often low, the heavy morning dews common above this altitude ensure an adequate supply of soil moisture.

As expected, the soils with higher nutrient status produced larger plants, up to three times heavier, with a higher proportion above ground. These plants also flowered earlier, produced more flowerheads and were generally taller with slightly larger leaves. It was, however, difficult to determine what effect soil nutrient status had on rhizome production because of the effect of soil bulk density. The lower bulk density soils produced plants with higher rhizome production, longer rhizomes, more rhizomes per plant and more daughter plants. The longer rhizomes were found to have longer internode lengths although the number of nodes exhibited a slight increase also. These results show clearly the effect of soil physical restriction on rhizome growth.

Branching of the rhizome system was found to be increased in the higher nutrient status, high bulk density soil. The rhizome systems produced

in this soil were short and densely branching while those produced in the lower bulk density soil were long and spindley with fewer branches. Although no measurements were taken it was also apparent that the few branches which were produced were smaller and exhibited less secondary branching. This apparent loss of apical dominance in the higher nutrient status and higher bulk density soil was probably attributable to the higher nutrient status. More specifically the nitrogen status, as shown by McIntrye (1972) in *Agropyron repens*. If nitrogen plays this important role then selection for improved nitrogen fixation may create plants with more branching. This branching may or may not be a desirable characteristic. For herbage production it is most likely that it would be undesirable, the rhizome system acting, even more so than at present, as an unnecessary photosynthesis sink diverting energy from potential herbage production during the initial few years of plant life.

The suspected low soil moisture status at the medium elevation site may explain the relatively good performances of the two diploids at this location (Table 12). As the diploids are reputed to be very hardy and drought tolerant (Barnard 1972, Bryant 1974), their performance at this location may be a reflection of their superior drought tolerance.

5.6.2 CLIMATE

The three locations used in the experiment varied in altitude from 12 m to 1200 m. a.s.l. and in distance by 100 km. The major climatic difference between the locations was temperature. The mean monthly maximum air temperatures for January decreasing from 22.8^{o}C at 12 m. a.s.l. to 14.8^{o}C at 1300 m. a.s.l., similarly the mean monthly minimum decreased from 12.5^{o}C to 5.9^{o}C for January. Frosts became more frequent at the higher altitude sites while monthly wind run was lower.

As both Paljor (1973) and Meares (1975) found that plants became smaller as temperature decreased, it was not surprising to find that total plant dry weight at the high altitude site was only one quarter of that produced in the similar soil at low altitude. In general, plants were smaller, had smaller leaves, flowered later and produced less flowerhead, and produced fewer, shorter rhizomes under the low temperature conditions at higher altitudes. As well as these differences the relative proportions of above ground dry weight, rhizome dry weight and root dry weight changed. Under high altitude conditions the proportion above ground dry weight and proportion rhizome dry weight were lower while the proportion root dry weight was higher. This result was similar to that of Paljor (1973) and Meares (1975) who both found that the 'root' : shoot ratio increased under low temperature conditions. Genotypes producing erect plants at the low altitude site were generally more prostrate under high altitude conditions, while leaf shape was relatively unaffected by environment.

5.7 GENOTYPE-ENVIRONMENT INTERACTIONS

As the majority of morphological characteristics measured did not exhibit genotype-environment interaction it should be possible to select morphologically uniform varieties under any environmental conditions. This would allow relatively quick results if highly fertile lowland sites were used.

Most of the production characteristics exhibited a high level of genotype-environment interaction. This necessitates that selection is performed under the environmental conditions, including grazing, in which the future cultivar is to be used. Also, if possible it would be desirable to select characteristics exhibiting low levels of genotype-environment

interaction. For example, the inheritance of the rhizome characteristics, dry weight, proportion dry weight, number, length and number of daughter plants were highly correlated. Presumably, selecting for an increase in one of these would increase the others as well. As both the number of rhizomes and the proportion rhizome dry weight exhibited no genotype-environment interaction. These two parameters should give the most useful response, adapted to a wider range of conditions. However, because of practical difficulties, in this case it would be easier to select rhizomatous types on the basis of daughter plant number, this would save digging up the plants and consequently allow more plants to be screened.

Genotype-environment interaction within the present varieties gives them a great deal of flexibility in their response to environmental conditions. This flexibility is of critical importance in the New Zealand high country where such harsh but fluctuating conditions are normal. Selecting 'superior' varieties with less genetic diversity and consequently less genotype-environment interaction could quite likely lower the flexibility of that variety, especially if it is not adequately-tested in the full range of conditions in which it is to be used.

It is apparent that genotype-environment interaction has been an insurance policy, in genetically diverse varieties, ensuring flexibility of response to a wide range of conditions, but by having this diversity, performance has been sacrificed. In selecting genetically uniform varieties it will be essential to test thoroughly their responses in the full range of conditions under which they are to be used to ensure adequate flexibility.

5.8 POTENTIAL FOR SELECTION

Selection response (R) is dependent on selection intensity, (S in

phenotypic standard deviation units), genetic variation (GCV%) and the square root of the narrow sense heritability estimate (h^2) (Burton and DeVane, 1953). This can be represented in the formula below:

$$R = S \times GCV\% \times \sqrt{h^2}$$

As both the population dependent factors, GCV% and h^2, have been estimated for numerous traits of *T. ambiguum* the selection response for any given selection intensity can be predicted. To do this, however, one has to assume that the broad sense heritability estimate is a good estimate of the narrow sense heritability.

For example, if a 5 percent selection intensity was used (S = 2.06 Burton and DeVane, 1953) on rhizome dry weight of cultivar Treeline (GCV% = 80, h^2 = .278) the selection response would be 87 percent. This implies that with one generation of selecting for increased rhizome dry weight it would be possible to increase the mean by 87 percent, an extremely high gain. Similarly, within cultivar Treeline the predicted responses to a 5 percent selection pressure for total plant dry weight would be 24 percent, above ground dry weight would be 48 percent and plant height, 62 percent. In general, for most plant parameters the selection responses ranges from 20 to 40 percent, very high gains made possible only through the exploitation of a large genetic variance.

Although it should be possible to make large gains in most parameters of *T. ambiguum* it is essential to know precisely what to select for. This of course, depends on the intended uses of the species. There are at present four geographical regions where *T. ambiguum* may have some use. Each of these regions requires cultivars adapted to their specific conditions. These four regions are:

1. The lowlands, where it could possibly be used for revegetation of roadsides and sand-dunes.
2. Dry South Island high country up to the treeline (1200 m), where there is considerable difficulty in finding a suitable pasture legume, also for revegetation purposes.
3. Moist South Island high country up to the treeline (1200 m), both as a pasture legume and for revegetation purposes.
4. Altitudes above the treeline (1200 m) where the only use would be for revegetation purposes.

For all these purposes it is essential that the cultivars developed have efficient nitrogen fixing abilities and are relatively easy to establish from seed. Other desirable characteristics depend on the potential uses.

For revegetation of lowland regions vigorous highly rhizomatous winter active forms are required. As Prairie was highly rhizomatous, with some plants exhibiting winter activity, it should be possible to select a cultivar from c.v. Prairie exhibiting the desired characteristics. Other hexaploid lines may also be suitable for this purpose, but the choice has to be made whether Prairie or some other line is used as Prairie can not cross with other hexaploid lines (Zorin *et al.* 1976a). For use on sand dunes, C.P.I. 57353 may offer some potential as a source of salt tolerance because it was reported to be adapted to salty soils (Zorin pers. comm.).

Although c.v. Treeline produced equivalent herbage in a pure stand as red clover, it is unlikely that *T. ambiguum* could produce this quantity until the stand becomes 'rhizome bound'. Until then, the rhizome system would act as a photosynthetic sink to the detriment of herbage production. Therefore the use of *T. ambiguum* as a special purpose pasture legume in lowland regions

is not envisaged.

As some of the lowland revegetation may be on a small scale allowing intensive methods it would be possible to plant cuttings. To do this it is suggested that about 20 cm square turfs, obtained using mechanical turf cutters, of a rhizomatous genotype of *T. ambiguum* would be placed about one metre apart across the area required. The use of cuttings would allow quicker establishment than from seed, and would allow the use of some highly vigorous rhizomatous genotypes which are presently available.

For the other three regions it is not known which characteristics to select, apart from herbage dry weight or rhizome dry weight for pastoral or revegetation uses respectively. To select cultivars suitable for these three regions it is envisaged that spaced - plants be established in these regions and the initial selection carried out on these. Of course, care would have to be taken to ensure that the plants were also adapted to grazing if they are for pastoral purposes. Presumably, for altitudes below the treeline cultivar Treeline would be suitable to select from. Above the treeline (1200 m) it is suggested that c.v. Treeline or c.v. Summit be used, but as the present experiment did not include this region these suggestions are purely speculative.

The other varieties, c.v. Forest, C.P.I. 51140 and C.P.I. 57353 did not appear to possess any additional qualities over c.v. Prairie, c.v. Treeline or c.v. Summit. However, it would be premature to disregard these other varieties, as they also offer good selection potential.

5.9 CRITICISM OF TECHNIQUES

Perhaps the major criticism of experiment one was that nodulation was

not scored. Although it was planned to visually score nodulation this was not performed because of the high rate of nodule loss while digging up and washing the plants. Also, it would have been a very difficult task to dig up and score plants under the arduous conditions, snow and high winds experienced at that time. As a general observation, however, most plants had fewer nodules than would be considered typical of white clover, while some had a high number of nodules. Leaf yellowing, typical of nitrogen deficiency, did not occur at any of the sites. However one Prairie genotype was permanently yellow even when grown in fertile potting mix, where it was nodulated.

The use of rhizome cuttings rather than seeds, although essential for the experimental design, may have affected the experiment in two ways. The first was that in the selection of genotypes for the experiment there would have been a bias towards rhizomatous plants as some parent plants did not possess sufficient rhizomes to produce in excess of 10 cuttings. This was particularly evident in the least rhizomatous cultivar, c.v. Summit. The second effect would be that the root systems of cuttings and seed could be different; seed grown plants may produce a larger taproot.

The use of only two replicates at each site was perhaps unwise. If at all possible, it would have been desirable to have three or more.

Because of the use of spaced plants it is not known how the species responds under sward conditions. Also, as the plants were only spaced 30 cm apart, rhizome growth, being unpredicably fast, meant that rhizomes were often intermingled, not a true spaced plant situation. What effect this had on the experiment is unknown.

The short term nature of the experiment, four months, may have biased the results, especially as no winter growth was included. Winter conditions are a very important limitation for plant growth in the New Zealand high country.

By the use of few very diver e environments in the experiment, the linear regression technique for comprehending genotype-environment interaction was not applicable. The inapplicability of this technique for environments with different limiting factors was foreseen by Knight (1970).

Overall, the experimental design appeared quite adequate as a preliminary investigation on a relatively unknown species. It would have been even more informative if the study could have been continued for more seasons.

5.10 RECOMMENDATION FOR FUTURE RESEARCH

Because of the wide range of genetic variation within each variety the differences between mean variety performances are not great. Therefore, there seems little point in comparing mean variety performances until more uniform varieties are obtained. It is recommended that selection for more uniform cultivars, either rhizomatous or herbage producing, be performed concurrently with the ability to fix nitrogen and for ease of establishment.

After more uniform and productive cultivars have been developed it would then be essential to evaluate their performance in long term field trials.

Other interesting topics for future research could be:

1. To look at how nitrogen status affects rhizome branching and the role played by nodulation in this relationship.

2. To evaluate genotypes of potential use in sand-dunes for salt tolerance.

3. To evaluate the sulphate requirements of different forms of the species. Presumably, having evolved in regions low in sulphate, some forms may have a low sulphate requirement.

4. To study the seasonal growth of the rhizome system. Does it grow predominantly in autumn when herbage production is low?

5. To look at the root system with reference to its fibrous or taprooted nature, especially in relation to seed grown plants and cuttings.

6. To investigate the movement of *Rhizobia* to daughter plants.

Another interesting trial would be to sow a mixture of red clover, or perhaps white clover and *T. ambiguum* in the hope that *T. ambiguum* would establish by the time red clover died out. This approach may offer a means of establishing a perennial pasture under high country conditions.

If selection was successful in *T. ambiguum* there is little reason why herbage yield could not be increased by 50 percent or more. This would make *T. ambiguum* as productive as and more persistent than white clover or *Lotus pedunculatus* in the New Zealand high country. Similarly, if selection of vigorous rhizomatous cultivars was successful, then *T. ambiguum* could play a very useful role in revegetation work.

5.11 CONCLUDING SUMMARY

A range of morphological, floral, rhizome, root and herbage characteristics were studied in order to fully describe the genetic variation and environmental response of six lines of *T. ambiguum*. For the genotypic evaluation, 30 genotypes of each line were clonally propagated into five edaphic and altitudinal sites. Plant growth, production and morphological

characters were measured on surviving plants after 4 months growth in each environment. Comparisons were also made with 'Huia' white clover and 'Maku' *Lotus pedunculatus* growing under the same conditions.

The polyploid lines were found to have larger leaves than the diploids, while all the *T. ambiguum* lines had larger leaves than white clover. The tetraploid lines were taller and had a more erect growth habit than the other two ploidy levels. In addition, the tetraploid line, C.P.I. 51140, had long narrow leaves while 40 percent of Treeline plants had a small proportion of leaves with more than three leaflets.

The diploids were found to flower earliest, followed by the tetraploids and lastly, the hexaploids. Tetraploid lines exhibited a very large variation in flowering date.

Cultivar 'Treeline' produced the most herbage under all the conditions, although not significantly more than C.P.I. 57353 or 'Prairie'. Similarly, it had the highest total plant dry weight. Although nodulation was not studied, it is suggested that a large portion of the variety and genotype differences may be due to differences in nodulation and nitrogen fixation.

None of the *T. ambiguum* lines produced as much herbage as did 'Huia' or 'Maku' at any site. However *T. ambiguum* did perform relatively better under harsher conditions. Because a larger proportion of *T. ambiguum* was below ground, the best *T. ambiguum* line, ('Treeline'), produced total plant dry matter equivalent to that of Maku and Huia at the high altitude site.

In the present trial 'Prairie' had the highest proportion of rhizomes, but, because Treeline had a higher total plant dry weight, the dry weight of rhizomes produced was similar for both varieties. The number of rhizomes,

number of daughter plants and rhizome dry weight were all highly correlated and these three characteristics exhibited similar trends among varieties. Rhizome length was found to increase with ploidy level as did rhizome internode length. However, the number of nodes was found to be higher in the diploids than the polyploids. Treeline was found to have a high proportion of branching nodes while C.P.I. 57353 and Summit had the lowest. Rhizome production appeared to be restricted in the soil of higher bulk density. In that soil, which was also the most fertile, rhizome branching was increased, indicating a partial loss of apical dominance. It is suggested that nitrogen supply was the main factor causing this, which may imply that well-nodulated plants have more rhizome branching.

'Prairie' had a lower proportion of roots than the other varieties, possibly due to their more fibrous nature. It is suggested that the high rhizome production of Prairie has developed at the expense of its root system.

It was shown using factor analysis that rhizome characteristics, herbage yield and flower production were not genetically correlated. However, morphological characteristics tended to increase in size with increasing herbage yields. The independence of rhizome and herbage characteristics would be of importance in developing rhizomatous cultivars with a reasonable degree of herbage production.

The polyploid varieties were found to be genetically more variable than the diploids. This was due either to intense selection, as in the diploid Summit, or to the increased genetic segregation and recombination possible in polyploids.

The estimate of heritability for morphological characteristics was generally between 40 and 70 percent, while agronomic characteristics, such as herbage and rhizome production, were generally between 20 and 30 percent. The number and dry weight of flowers had low heritabilities, around 10 percent, indicating a large environmental influence.

Genetic variation within each line was generally much higher than the variation between lines. This had the effect of cancelling out variety differences. It is apparent that a higher gain in performance could be obtained by selecting within a line than by screening different lines in search of agronomic quality. It is recommended that 'Prairie' be used as a basis for selecting a highly rhizomatous cultivar while 'Treeline' could be used as a basis for a cultivar with higher herbage production. Nevertheless, other varieties used in this experiment also have useful characteristics and might yield future cultivars.

In a second experiment, an established stand of cultivar 'Treeline' produced equivalent to 13250 kg ha^{-1} of herbage during one good growing season. To produce this the plots were irrigated and cut to ground level every two months. Cutting every month appeared to deplete plant reserves indicating that to obtain maximum production this cultivar of *T. ambiguum* requires a long growing interval. It was also shown that root and rhizome yield could reach equivalent to 12600 kg ha^{-1} allowing a massive storage of energy and assimulates for the sward. Whether the herbage production obtained was using up these reserves is unknown. Seed yields were found to reach 500 - 700 kg ha^{-1} equivalent indicating that adequate seed yields can be obtained.

The results were discussed in relation to earlier observations on *T. ambiguum* by workers in Russia, Australia, U.S.A. and New Zealand. Suggestions were made for further genetic and agronomic testing.

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APPENDIX A

Soil and Climate Data

Soil Analysis Values

Meteorological Data Lincoln College 12 m. a.s.l.

Meteorological Data Craigieburn Forest 914 m. a.s.l.

Temperature 1300 m. a.s.l. Mt Cheesman

Meteorological Data Craigieburn Ski Basin 1555 m. a.s.l.

Meteorological Data Rangiora 36 m. a.s.l.

Table 30: Soil Analysis Values

	pH	Olsen P	Troug P	Total P	Total N	Ca	K	Mg	P Retention	SO_4.S	Bulk Density	Water Holding Capacity
Cass 0-15 cm	5.4	9	1.3	1.2 mg %	0.38 %	2	5	6	66%	9ppm	0.73	92%
Cass 0-15 cm + fertiliser	5.3	20	-	-	-	3	7	10	-	-	-	-
Cass 15-30 cm	5.3	9	-	-	-	2	3	3	-	-	-	-
Bealey 0-15 cm	5.0	9	-	-	-	2	4	5	52%	-	0.71	-
Bealey 0-15 cm + fertiliser	4.6	36	-	-	-	3	5	12	-	-	-	-
Wakanui 0-15 cm	5.8	140	-	-	-	13	26	46	-	-	1.58	-
Wakanui 15-30 cm	5.9	15	-	-	-	7	13	15	-	-	-	-

Olsen P <20 response likely >35 response unlikely
Ca desirable level about 7
K <3 response expected 3-5 test strip 6+ unlikely response
Mg <3 response in herbage <10 herbage content should increase (stock health)

Table 31: Meteorological data Lincoln College 12 m.a.s.l.

Month 1977/78	Mean Cloud Cover (eights)	Ground Frost Days	Rain Days >1.0mm	Rainfall mm	Humidity %	Mean Max °C	Mean Min °C	Abs Max °C	Abs Min °C	Mean Grass Min °C	Total Sunshine Hours	Total Wind Run (km)	Total Pan Evaporation mm
November	4.4	4	5	29.0	62.6	18.4	6.6	26.4	1.3	4.0	220.1*	12100	181.8
December	4.7	1	7	48.8	73.6	21.1	8.4	30.9	3.8	5.1	191.9	11223	215.1
January	5.5	0	6	43.2	78.2	22.8	12.5	31.8	5.8	10.3	205.2	13191	238.2
February	4.3	0	2	19.9	77.2	23.2	12.0	33.5	6.9	8.8	230.1	11036	200.8
March	4.5	1	3	26.8	78.0	22.4	10.5	29.9	1.7	7.8	198.8	12630	180.4

* first 2 days missing

Table 32: Meteorological data Craigieburn Forest 914 m.a.s.l.

Month 1977/78	Mean Cloud Cover (eights)	Ground Frost Days	Rain Days >1.0mm	Rainfall mm	Humidity Mean %	Temperature °C					Solar Radiation (Langleys)	Total Wind Run (km)	Total Pan Evaporation mm
						Mean Max	Mean Min	Abs Max	Abs Max	Mean Grass Min			
November	5.2	11	9	101.2	68.4	15.2	3.0	25.3	-1.6	0.3	15197	4787	25.4
December	4.7	5	15	120.1	66.6	17.1	5.0	26.2	-0.8	2.5	14269	4759	89.7
January	4.5	1	7	56.9	79.7	21.3	8.5	26.8	-0.7	6.2	14049	4525	224.7
February	2.6	0	4	8.6	72.0	23.1	8.1	29.3	3.8	4.3	12506	3838	121.8
March	4.0	5	7	97.8	68.3	20.1	6.3	28.0	-2.0	3.3	11107	4531	103.9

Table 33: Temperatures 1300m a.s.l. Mt. Cheeseman

1977-78 Month	Mean Max ^{o}C	Mean Min ^{o}C	Abs Max ^{o}C	Abs Min ^{o}C
November	9.6	1.9	18	-3
December	10.9	4.1	20	1
January	14.8	5.9	21	1
February	12.1	8.9	21	4
March	11.0	5.9	21	-1

Table 34: Meteorological data Craigieburn Ski Basin 1555 m.a.s.l.

Month 1977/78	Mean Cloud Cover (eights)	Ground Frost Days	Rain Days >1.0mm	Rainfall mm	Humidity Mean %	Temperature °C					Total Wind Run (km)
						Mean Max.	Mean Min.	Abs Max.	Abs Min.	Mean Grass Min	
November	5.7	19	-	-	-	7.5	2.0	17.0	-5.6	-2.0	9142
December	6.0	19	14	148.2	71.0	10.7	2.0	18.3	-0.5	1.0	8780
January	4.7	7	7	87.2	62.3	16.9	5.9	19.7	-2.2	2.8	7602
February	3.2	4	6	31.0	62.6	15.4	6.5	20.5	0.1	3.1	7363
March	4.6	12	8	138.0	60.0	12.8	4.7	22.4	-5.5	1.2	9155

Table 35: Meteorological Data Rangiora 36m a.s.l. 1977-78

Month	Mean Grass Min ^{o}C	Rainfall mm	No. of ground frosts
August	-1.9	76.0	18
September	1.5	95.4	7
October	3.7	26.1	4
November	4.1	31.4	3
December	7.2	48.9	0
January	10.3	47.4	0
February	9.5	15.2	0
March	8.1	23.0	0
April	8.4	268.9	0
May	3.6	28.9	5
June	0.8	91.4	12
July	0.7	171.7	10
August	0.4	56.8	16

APPENDIX B

Presentation of Variety Means and Analyses of Variance not presented in results.

- Total number of plants used in the analysis.
- Variety means for:
  proportion above ground dry weight
  green weight of petiole
  green weight of leaf
  air dry weight of flowers per plant
  Mean air dry weight of flowerheads.
- Mean flowering dates for Huia and Maku
- Maximum values for any plant for each variety for:
  number of flowers
  rhizome length
  number of rhizomes
  number of daughter plants
  proportion rhizomes
- Ranges of Total dry weight and above ground dry weight for each variety.
- Analysis of Variance for all characteristics.
- Photocopy of multiple leaflets.

Table 36: Total number of plants used in the analysis, for each variety at each environment

		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high	Number of Genotypes
Forest	2x	58	58	58	58	58	29
Summit	2x	44	41	37	36	43	22
51140	4x	60	58	58	56	58	30
Treeline	4x	54	47	53	52	51	27
57353	6x	56	53	56	55	56	28
Prairie	6x	58	58	58	58	58	29
Huia		13	13	13	13	13	5
Maku		13	13	13	13	13	6

Table 37: Proportion of dryweight above ground, variety means at all environments.

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	.51 d	.31 d	.44 bc	.29 cd	.27 d
Summit	2x	.53 c	.40 c	.52 b	.33 c	.33 c
51140	4x	.48 cde	.28 d	.39 cd	.27 cd	.20 e
Treeline	4x	.40 e	.26 d	.38 cd	.25 cd	.23 de
57353	6x	.45 cde	.28 d	.39 d	.24 d	.23 de
Prairie	6x	.43 de	.26 d	.34 d	.24 d	.22 de
Maku		.75 b	.74 b	.53 b	.53 b	.68 b
Huia		.91a	.83a	.67a	.67a	.75a
SLSD (5%)		.087	.065	.091	.080	.054

Variety means within any environment with the same letter beside are not significantly different using Scheffe's Least Significant Difference at the 5% level (SLSD(5%)).

Table 38:

a) Mean flowering dates of Maku and Huia at each environment

	Environment (Soil/altitude)				
	Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Huia	11 Nov	25 Nov	24 Dec	6 Dec	17 Dec
Maku	13 Dec	7 Jan	1 Feb	29 Jan	8 Feb

b) Mean flower dry weight per flowering plant (g) and mean dry weight per flowerhead (g), variety means at the two Lincoln College environment

		Flower dry weight (g)		Dry Weight per flowerhead (g)	
		Wak/low	Cass/low	Wak/low	Cass/low
Forest	2x	7.08	0.99	0.20	0.14
Summit	2x	6.08	1.18	0.19	0.11
51140	4x	8.38	1.06	0.20	0.14
Treeline	4x	6.28	0.49	0.16	0.09
57353	6x	9.59	0.67	0.27	0.17
Prairie	6x	9.09	1.01	0.22	0.13

c) Green weight of petiole and leaf (g), variety means at the two Lincoln College environments

		Weight of Petiole (g)		Weight of Leaf (g)	
		Wak/low	Cass/low	Wak/low	Cass/low
Forest	2x	.10	.08	.23	.19
Summit	2x	.08	.08	.20	.18
51140	4x	.14	.11	.30	.25
Treeline	4x	.19	.17	.29	.27
57353	6x	.24	.16	.48	.39
Prairie	6x	.16	.11	.35	.26

Table 39: Maximum number of flowers on any plant of a given variety at each environment.

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	101	24	37	10	6
Summit	2x	90	35	55	10	9
51140	4x	149	21	47	10	7
Treeline	4x	163	23	51	13	15
57353	6x	176	13	31	4	8
Prairie	6x	150	21	50	5	6

No significance test possible as these were unreplicated results.

Table 40: Maximum rhizome lengths (cm) of any plant of each variety at all environments.

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	47	56	24	39	30
Summit	2x	44	47	31	37	24
51140	4x	51	82	35	78	35
Treeline	4x	50	55	28	39	33
57353	6x	64	85	36	67	34
Prairie	6x	61	70	31	52	39

No significance test possible as these were unreplicated results.

Table 41: Maximum number of rhizomes of each variety at all environments.

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	37	26	38	23	26
Summit	2x	36	16	15	11	8
51140	4x	57	16	12	12	9
Treeline	4x	78	38	46	18	28
57353	6x	31	21	12	12	10
Prairie	6x	69	22	16	18	25

No significance test possible as these were unreplicated results.

Table 42: Maximum number of daughter plants for each variety at all environments.

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	19	5	7	5	3
Summit	2x	12	5	2	2	2
51140	4x	32	7	4	7	6
Treeline	4x	41	21	6	4	4
57353	6x	17	7	7	13	5
Prairie	6x	61	7	4	8	4

No significance test possible as these were unreplicated results.

Table 43: Maximum proportion rhizome dry weight (percentage) of all varieties at all environments.

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	39	65	53	59	68
Summit	2x	23	37	24	51	41
51140	4x	44	63	42	66	50
Treeline	4x	57	73	49	62	53
57353	6x	49	62	34	68	52
Prairie	6x	62	64	55	61	51

No significance test possible as these were unreplicated results.

Table 44: Ranges of Total Plant Dry Weight relative to Treeline mean, for all varieties at all environments.

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	26-109	20-142	20-159	30-148	9-121
Summit	2x	16- 92	8-107	19-170	17-136	15-153
51140	4x	8-236	12-131	14-289	6-141	16-152
Treeline	4x	28-212	40-218	25-200	42-171	27-244
57353	6x	18-199	10-153	5-271	9-227	27-183
Prairie	6x	20-189	6-172	3-189	30-162	8-279
Maku	mean	171	186	66	119	105
Huia	mean	215	225	270	115	88
Treeline (g)		56.7	20.6	16.9	6.4	5.7

Table 45: Ranges of Above Ground Dry Weight, relative to Treeline mean, of all varieties at all sites.

Variety	Ploidy	Environment (Soil/Altitude)				
		Wak/low	Cass/low	Wak/med	Cass/med	Bealey/high
Forest	2x	22-120	19-178	8-260	30-236	13-178
Summit	2x	17-113	9-168	20-211	13-267	11-210
51140	4x	5-257	9-169	3-369	9-248	11-166
Treeline	4x	19-281	25-202	12-289	31-239	29-596
57353	6x	7-285	12-175	2-493	11-247	11-185
Prairie	6x	15-242	4-178	1-309	28-182	9-360
Maku mean		386	545	135	253	289
Huia mean		595	744	615	305	267
Treeline mean (g)		18.74	5.17	6.57	1.60	1.40

Table 46: Weighted analysis of variance for seven characteristics of 165 *Trifolium ambiguum* genotypes

Source	d.f.	Mean Square						
		Top D.W.	Rhizome D.W.	Root D.W.	Total D.W.	Number of flowers	Plant Height	Leaflet Length
Genotypes	164	3.7**	4.7**	5.1**	4.7**	0.27**	6.6**	7.1**
Environment	4	35.7**	19.5**	16.6**	64.7**	9.88**	155.3**	9.3**
Soil	1	101.5**	30.4**	43.4**	153.6**	18.93**	42.4**	8.2**
Climate	1	15.5**	0.4NS	19.4**	35.9**	21.27**	366.2**	7.8**
Soil x Climate	1	27.4**	50.1**	1.8NS	83.4**	0.79**	123.9**	0.68NS
Genotype x environment	656	1.4**	1.2**	1.1*	1.2**	0.13**	0.72NS	0.58**
Genotype x Soil	164	1.5*	1.4**	1.2*	1.3**	0.12**	).75NS	0.63**
Genotype x Climate	164	1.5*	1.2**	1.2*	1.3**	0.11*	0.76NS	0.66**
GxSxC	164	1.3*	1.1**	1.1NS	1.1**	0.16**	0.75NS	0.55*
Residual error	778	1.04	0.74	0.93	0.79	0.092	0.64	0.45
Coefficient of Variation		53.4	74.0	44.4	37.1	23.5	28.4	15.6

* significant differences at 0.05 probability

** significant differences at 0.01 probability

N.S. no significant differences observed

Table 47: Analysis of Variance (Mean Square)

Characteristic	Genotype	Environment	Interaction	Error	
Degrees of Freedom	164	4	656	778	
Rhizome length	4.54 **	66.82 **	1.23 *	1.04	W
Daughter plants	0.44 **	5.53 **	0.21 *	0.17	W
Plant width	4.31 **	57.39 **	1.29 *	1.02	W
Leaf width	6.34 **	28.38 **	0.78 *	0.61	W
Proportion above ground P.W.	0.0387**	2.9284**	0.110 **	0.0074	R
Proportion root D.W.	0.059 **	2.632 **	0.016 *	0.013	R
Number of rhizomes	0.45 **	2.95 **	0.09 NS	0.09	W.S
Petiole length	5.12 **	74.77 **	1.08 NS	1.03	W.
Proportion rhizome D.W.	0.088 **	1.174 **	0.019 NS	0.18	R.
Leaf length/width	2.17 **	0.29 *	0.08 NS	0.10	R
Height width	5.69 **	164.42 **	0.95 NS	0.92	W.
Degrees of Freedom	164	1	164	314	
Leaf area	61.7 **	200.2 **	13.33 NS	11.48	R.
Vegetative Top D.W.	2.71 **	15.50 **	1.11 **	0.69	W.
Flower weight/plant	2.12 **	60.31 **	1.71 **	1.16	W.
Petiole green weight	0.019 **	0.202 **	0.004 NS	0.004	R.
Leaf green weight	0.047 **	0.434 **	0.007 NS	0.007	R.
Proportion flower weight	0.017 **	2.946 **	0.008 NS	0.007	R.
Proportion Veg. Top D.W.	0.0081**	0.7491**	0.0043*	0.0029	R.
Weight/cm petiole	.0005**	.0086**	.0001NS	.0001	R.
Weight/cm^2 leaf area	.030 **	.700 **	.009 NS	.007	R.
Degrees of Freedom	138	1	138	197	
Number of nodes	0.67 **	7.63 **	0.34 NS	0.31	S.
Mean internode length	0.77 **	49.86 **	0.25 NS	0.24	R.
Rhizome branching	0.16 **	1.28 **	0.09 NS	0.11	A.

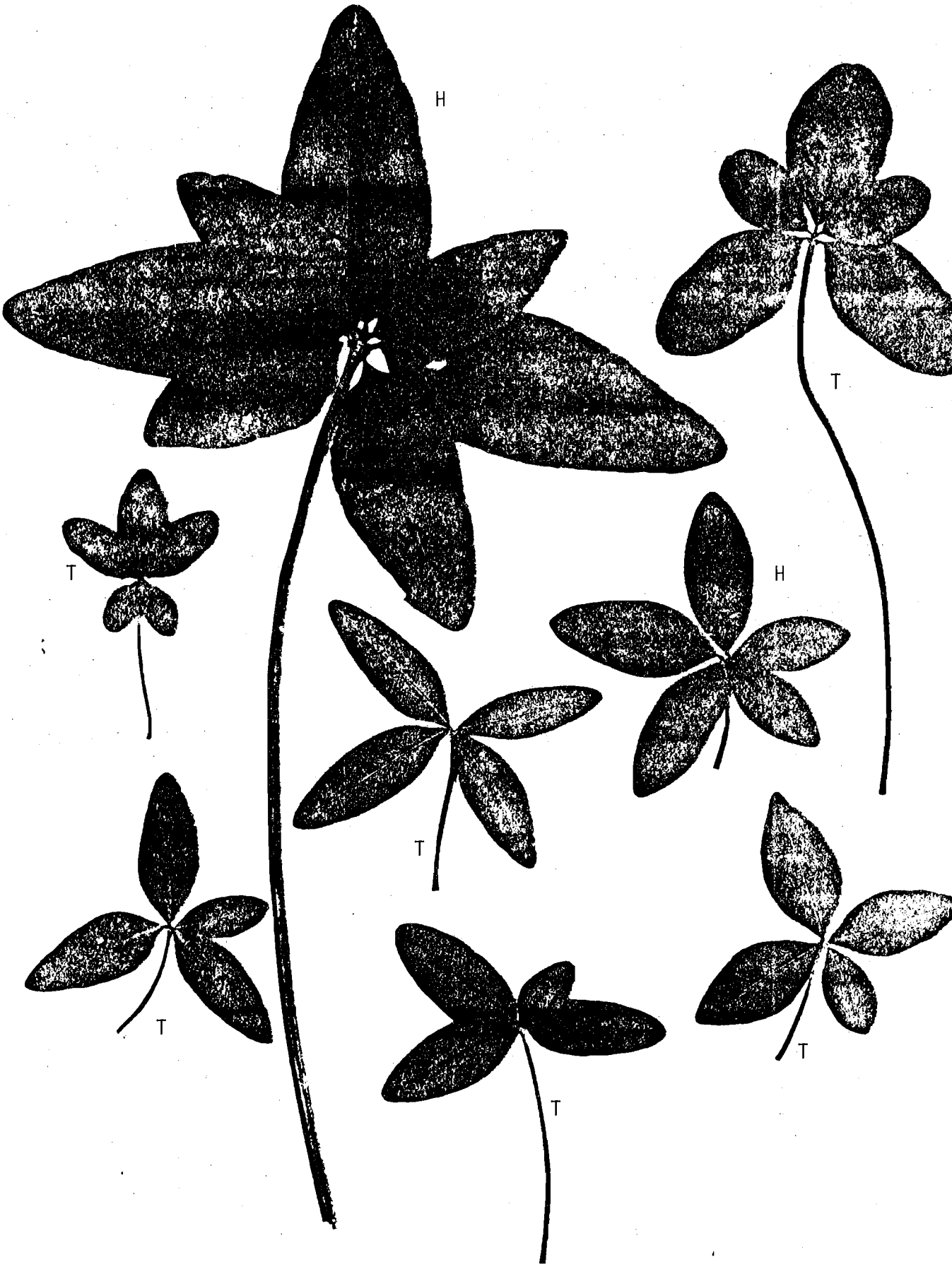
** significant 0.01
* significant 0.05
NS not significant at 0.05

W weighted analysis of variance
R analysis of variance on raw data
S square root transformation
A arcsue transformation

Photocopy of Multiple Leaflets

T = Treeline

H = 57353



APPENDIX C

Computer Programs

GXE - description

Use of GXE

Program listing

Example output

GENCOR - description

Use of GENCOR

Program listing

Example output

GXE - description

A program written for analysis of genotype environment interaction experiments (n genotypes completely randomised within m environments). Performs the following calculations:

Analaysis of Variance for equal and unequal replicates according to fixed and random effects models.

Partitions up Analysis of Variance into genetic components of variance. Calculates broad sense heritability estimates and their SE. (See statistical material and methods).

Tests for homogeneity of variance (Bartlet's test) and whether environments have differing error variances (Bartlet's test).

Calculates grand mean, coefficient of variation and standard deviation of genotype means in each environment.

Regression analysis:

1. of each genotype on mean of all genotypes.
2. of each genotype on a measure read in after the "MEASURE" card.

calculates mean, slope, tests if slope different to 1.0, calculates SE of slope, Y intercept, r^2 of regression line, probability of regression, Hanson's stability parameter (Hanson 1970).

Calculates heterogeneity of regression, heterogeneity of deviation from regression and convergence after Eagles *et. al.* (1977).

N.B. In the use of the program it may be necessary to alter the Dimensions of the "D" (data) array and "N" (replicates) array to accommodate different experimental designs.

Instructions for use of GXE

Explaining necessary cards and functions of each.

TITLE ...	a card containing any title for print out, optional.
GENOTYPES n	number of genotypes (n)
ENVIRONMENTS m	number of environments (m)
	the order of the above two cards determines the order for reading in data and the number of replicates, first card iterates the slowest.
REPLICATES = ℓ *	where ℓ equals the number of replicates. If unequal replicates the number of replicates are separated by commers starting on the next card in the order determined by the order of GENOTYPES and ENVIRONMENT card.
READ m	reads m variables, default value of 1, optional
USE n	uses the nth variable for analysis, optional, default = 1.
TRANSFORM n	transorms data, where n = 0 to 6.
	0 = raw data 1 = square root $(\bar{x}+1)$ 2 = $\log_e (x+1)$
	3 = $\log_{10}(x+1)$ 4 = $1/(x+1)$ 5 = arcsine (x)
	6 = arcsine (x/100)
GNAME	followed by genotype names starting next card, format 10A6, optional.
ENAME	followed by environment names starting next card, format 10A6, optional.
ALPHA n	where n is the value of alpha for Hanson's stability parameter, between 0.0 and 1.0, format F3.2 optional.
MEASURE	followed by values of environmental measures, if means are not used for regression, free format, separated by commers, starting on next card, optional.

* presence of equals sign signifies equal replicates

SUPPRESS	suppresses the regression analysis, automatic if the number of environments less than or equal to 2. Therefore previous 4 cards unnecessary.
FILE	reads binary data from disc file number 3, optional
COLUMN	reads data in column format, one observation of each variate per card.
FREE	reads data in free format, separated by commers.
FIXED	reads data in fixed format, format specified.
	One of the above three cards is essential.
FORMAT	includes format for fixed format, optional.
DATA	essential card, followed by data check order of instructions from READ until FORMAT not important.

```
      FILE  3(TITLE="MYFILE.",KIND=DISK)
      C
      C     READ IN ALL THE AVAILABLE OPTIONS
      C
            DIMENSION Z(25),AVEG(200),GNAME(200),ENAME(25),WEIGHT(25),
           *NOD(25),AVEE(25),D(5,200,10),N(201,10)
            DIMENSION IB(76),IFORM(74)
            COMMON /A/NGEN/B/NENV/E/ALPHA/F/MAXREP/G/NGEN1/H/NREAD
           */I/NUSE/K/NTRAN/L/MEASUR/M/IFILE,IFAST/N/INPUT/O/NSUPP
            DO 59 I=1,200
           59 GNAME(I)="        "
            DO 60 J=1,25
           60 ENAME(J)="        "
            NREAD=1
            NUSE=1
            MAXREP=0
          100 A="    "
            DO 50 I=1,76
           50 IB(I)=" "
            READ(5,1)A,(IB(I),I=1,76)

            1 FORMAT(A4,76A1)
              IF(A.IS."TITL") WRITE(6,2) A,(IB(I),I=1,76)

            2 FORMAT(26X,A4,76A1,/26X,80('*'),//)
              IF(A.IS."TITL") GO TO 100
              IF(A.IS."GENO")NGEN=NUMB(IB,76)
              IF(A.IS."GENO") IFAST=0
              IF(A.IS."GENO") WRITE(6,200)NGEN
          200 FORMAT(1X,'THE NUMBER OF GENOTYPES EQUALS ',I6)
              IF(A.IS."GENO") NGEN1=NGEN + 1
              IF(A.IS."GENO") GO TO 100
              IF(A.IS."ENVI") NENV=NUMB(IB,76)
              IF(A.IS."ENVI") IFAST=1
              IF(A.IS."ENVI") WRITE(6,201)NENV
          201 FORMAT(1X,'THE NUMBER OF ENVIRONMENTS EQUALS ',I6)
              IF(A.IS."ENVI") GO TO 100
              IF(A.IS."REPL") GO TO 10
              GO TO 20
           10 DO 51 J=1,76
              IF(IB(J).IS."=") WRITE(6,202)
          202 FORMAT(1X,'THERE ARE EQUAL NUMBER OF REPLICATES')
           51 IF(IB(J).IS."=") MAXREP=NUMB(IB,76)
              CALL READR(A)
              IF(A.IS."REPL") GO TO 100
           20 IF(A.IS."READ")  NREAD=NUMB(IB,76)
              IF(A.IS."READ") GO TO 100
              IF(A.IS."USE ") NUSE=NUMB(IB,76)
              IF(A.IS."USE ") GO TO 100
              IF(A.IS."TRAN") NTRAN=NUMB(IB,76)
              IF(A.IS."TRAN") GO TO 100
              IF(A.IS."ALPH") ALPHA=NUMB(IB,76)/100.
              IF(A.IS."ALPH") WRITE(6,13) ALPHA
           13 FORMAT(1X,'ALPHA =',F6.3)
              IF(A.IS."ALPH") GO TO 100
              IF(A.IS."FILE") IFILE=3
              IF(A.IS."FILE") GO TO 100
              IF(A.IS."COLU") INPUT=3
              IF(A.IS."COLU") GO TO 100
              IF(A.IS."FIXE") INPUT=2
              IF(A.IS."FIXE") GO TO 100
              IF(A.IS."FREE") INPUT=1
              IF(A.IS."FREE") GO TO 100
              IF(A.IS."GNAM") READ(5,7)(GNAME(I),I=1,NGEN)
              IF(A.IS."GNAM") GO TO 100
              IF(A.IS."ENAM") READ(5,7)(ENAME(I),I=1,NENV)
              IF(A.IS."ENAM") GO TO 100
            7 FORMAT(10A6)
              IF(A.IS."MEAS") READ(5,/)(Z(J),J=1,NENV)
              IF(A.IS."MEAS") WRITE(6,204)
          204 FORMAT(1X,'THE ENVIRONMENTAL MEASURES ARE READ IN ,NORMALLY THE EN
             *VIRONMENTAL MEANS ARE USED.'//1X,'THE MEASURES USED INSTEAD ARE')
              IF(A.IS."MEAS") WRITE(6,205) (Z(J),J=1,NENV)
          205 FORMAT(1X,10F12.4)
              IF(A.IS."MEAS") GO TO 100
              IF(A.IS."SUPP") NSUPP=10
              IF(A.IS."SUPP") GO TO 100
              IF(A.IS."FORM") GO TO 25
              GO TO 35
           25 DO 55 I=1,74
           55 IFORM(I)=IB(I+2)
              GO TO 100
           35 IF(A.IS."DATA") IDATA=1
              IF(IDATA.EQ.0) GO TO 207
              IF(NENV.LE.2) NSUPP=10
      C
      CC    CALL THE MAIN PROGRAM FOR CALCULATIONS TO BEGIN
      C
            CALL MAIN(WEIGHT,GNAME,ENAME,NOD,AVEE,D,N,AVEG,Z,IFORM)
            STOP
          207 WRITE(6,9)
            9 FORMAT(1X,'MISSING DATA CARD'20X,'ERROR')
              STOP
              END
```

```
C
C     THIS SUBROUTINE IS THE MAIN PART OF THE PROGRAM
C
      SUBROUTINE MAIN(WEIGHT,GNAME,ENAME,NOD,AVEF,D,N,AVEG,Z,IFORM)
      COMMON /A/NGEN/B/NENV/C/KMEAN/D/ENVAVE/E/ALPHA/F/MAXREP/G/NGEN1
     */L/MEASUR/K/KTRAN/O/PSHPP
      DIMENSION NOD(9),SS(9),XMS(9),FF(9),F(9),PP(9),P(9),ANOVA(9,5),
     *CUM(13),IFORM(74)
      DIMENSION WEIGHT(NENV),GNAME(NGEN),ENAME(NENV),NOD(NENV),
     *  AVEF(NENV),D(MAXREP,NGEN,NENV),N(NGEN1,NENV),AVEG(NGEN),Z(NENV)
      DATA ANOVA/'SOURCE','ENVIRO','INTERA','  WITH','    ','    ','RESI','E
     1RROR','TOTAL','PES','NMENTS','CTION','ROGENE','  CONV','  NONC','D
     2UAL','  WITH','PES','    ','    ','(G X E','ITY OF','ERGENC','ONVERG','  ',
     3'N REPL','    ','    ','    ','    ',')',' REGRE','E','ENCE','    ','ICATES','    ','  ',
     4'    ','    ','SSIONS','    ','    ','    ','    ','    ','    ','    '/
      DO 77 I=1,9
      P(I)='    '
   77 PP(I)='    '
      GEN=NGEN
      ENV=NENV
C
C     CALL THE SUBROUTINE TO READ IN ALL THE DATA
C
C     CALL THE SUBROUTINE TO TRANSFORM THE DATA
C
      CALL READE(IFORM,D,N)
      CALL TRANSF(KTRAN,D,N)
C                                                 THE J DO LOOP
      SSQU=0.0
      SSQE=0.0
      NO=0
      RECNO=0.0
      RECDF=0.0
      KSUM=1
      KSSQ=2
      KMEAN=3
      NODF=0
      DO 73 I=1,13
   73 CUM(I)=0.0
      EAVE=0.0
      TOTAL=0.0
      NOT=0
      ISUM=NGEN + 1
C                                 SUM OF SQUARES OF REPS IS STORED IN KSSQ
C                                 THE SUM OF REPS ARE STORED IN KSUM
C                                       TOTAL=TOTAL SUM OVER ALL
C                                       SSQU=TOTAL-SUM OF SQUARES
C                                       SSQE =SUM OF SQUARE ENVIRONMENTS
C                                       AVEF(J)=MEAN OF J ENVIRONMENT
C                                       NO=TOTAL NO INDIVIDUALS
      DO 50 J=1,NENV
       AVEF(J)=0.0
       CUM(11)=0
       N(ISUM,J)=0
       NOD(J)=0
       DO 51 I=1,NGEN
        SUM=0.0
        SSQ=0.0
        DO 53 K=1,D(I,J)
         SUM=SUM+D(K,I,J)
         SSQ=SSQ+(D(K,I,J)**2)
   53   CONTINUE
        D(KMEAN,I,J)=SUM/D(I,J)
        D(KSUM,I,J)=SUM
        D(KSSQ,I,J)=SSQ
        SSQU=SSQU+SSQ
        AVEF(J)=AVEF(J) + D(KMEAN,I,J)
        CUM(11) =CUM(11) + D(KMEAN,I,J)*D(KMEAN,I,J)
        TOTAL=TOTAL+SUM
        NO=NO + D(I,J)
        RECNO=RECNO + 1.0/D(I,J)
        N(ISUM,J)=N(ISUM,J) + N(I,J)
        IF(D(I,J).LE.1) GO TO 51
        VAR=(D(KSSQ,I,J) - ((D(KSUM,I,J)**2)/N(I,J)))
        VAR=VAR/(D(I,J)-1)+1
        CUM(1)=CUM(1) + ALOG(VAR)*(N(I,J)-1)
        CUM(2)=CUM(2) + VAR
        NOD(J)=NOD(J) + 1
        NOT=NOT + N(I,J) - 1
        RECDF=RECDF + 1.0/(D(I,J)-1)
   51   CONTINUE
        SSQE=SSQE+AVEF(J)**2/GEN
        WEIGHT(J)=SQRT((CUM(11)-AVEF(J)*AVEF(J)/GEN)/(GEN-1.))
        AVEF(J)=AVEF(J)/GEN
        EAVE=EAVE + AVEF(J)
        NODF=NODF+NOD(J)
   50 CONTINUE
```

```
C
C     ******************************************************************
C                              HOMOGENEITY OF VARIANCE
      MDF=MODE-1
      CHI=ALOG(CUM(2)/MODE)*NOT-CUM(1)
      CHI=CHI/(1.+(1./(3.*(MODE-1.))*(RECDF-1./NOT)))
      PROB=FISHER(CDF,10000,CHI/MDF)
      WRITE(6,16) MDF,CHI,PROB
   16 FORMAT(1X,////26X,'HOMOGENEITY OF VARIANCE',12X,'(BARTLETS TEST)',
     */26X,23('*'),//1X,'DF ',I6,'  CHI-SQUARE ',F17.3,6X,'PROBABILITY',
     *2X,A6,/)
C
C     ******************************************************************
C                                                    THE 1 DO LOOP
      GSSQ=0.0
      SSQUT=0.0
C                                        AVEG(I)=MEAN OF 1 GENOTYPE
C                                       GSSQ=SUM OF SQUARES FOR GENOTYPE
C                              SSQUT=SUM OF SQUARES FOR INTERACTION
      DO 56 I=1,NGEN
       SUM=0.0
       DO 57 J=1,NENV
        SUM=SUM+D(KMEAN,I,J)
        SSQUT=SSQUT+ D(KMEAN,I,J)*D(KMEAN,I,J)
   57  CONTINUE
       AVEG(I)=SUM/ENV
       GSSQ=GSSQ+ SUM*SUM/ENV
   56 CONTINUE
C
C     ******************************************************************
C                                    CALCULATION OF ANOVA TABLE VALUES
      HARMEN=1./((1./(ENV*GEN))*RECNO)
      CF=(EAVE*NGEN)**2/(ENV*GEN)
C                                          CF=CORRECTION FACTOR
C     EAVE=EAVE/NENV
C                              EAVE=MEAN GENOTYPE RESPONCE, ALL ENVIRONMENTS
      SS(9)=SSQU-TOTAL**2/NO
      SS(1)=(GSSQ-CF)
      SS(2)=(SSQE-CF)
      SS(3)=(SSQUT-CF-SS(1)-SS(2)) * HARMEN
      SS(1)=SS(1) * HARMEN
      SS(2)=SS(2) * HARMEN
      MODF(1)=NGEN-1
      MODF(2)=NENV-1
      MODF(3)=MODF(1)*MODF(2)
      MODF(9)=NO-1
      MODF(8)=MODF(9)-MODF(1)-MODF(2)-MODF(3)
      SS(8)=SS(9)-(SS(1)+SS(2)+SS(3))
      XMS(8)=SS(8)/MODF(8)
C
C     ******************************************************************
C                                    ENVIRONMENTAL MEANS
      DO 72 I=1,10
   72  CUM(I)=0.0
      ENVDF=0.0
      NOT=0
      WRITE(6,27)
   27 FORMAT(1X,25X,'ENVIRONMENTAL MEANS',/26X,19('*'),//)
      DO 62 J=1,NENV
       WRITE(6,31) J,ENAME(J),AVEE(J),WEIGHT(J)
   31  FORMAT(1X,'MEAN OF ENVIRONMENT ',I2,' (',A6,')',' IS ',7X,F12.6,6X
     *,'SD OF GENOTYPE MEANS = ',F15.6)
       CUM(7)=CUM(7) + ALOG(WEIGHT(J)*WEIGHT(J))*(N(ISUM,J)-1)
       CUM(8)=CUM(8) + WEIGHT(J)* WEIGHT(J)
       NOT=NOT + N(ISUM,J)-1
       ENVDF=ENVDF + 1.0/(N(ISUM,J)-1)
   62 CONTINUE
      HR=SQRT(XMS(8))/EAVE *100
      WRITE(6,32)EAVE,HR
   32 FORMAT(1X,'GRAND MEAN',29X,F14.6,/1Y,'COEFFICIENT OF VARIATION',13
     *X,F12.2,'%',///)
      CHI=ALOG(CUM(8)/ERV)*NOT-CUM(7)
      CHI=CHI/(1.+(1./(3.*(ENV-1.))*(ENVDF-1./NOT)))
      PROB=FISHER(MODF(2),10000,CHI/MODF(2))
      WRITE(6,29)CHI,MODF(2),PROB
   29 FORMAT(1X,'DO THE ENVIRONMENTS HAVE DIFFERENT ERROR VARIANCES',/1X
     *,'CHI SQUARE',F12.3,' AT ',I4,' DF',6X,'PROBABILITY',2X,A6,//)
      IF(USUPP.EQ.10) GO TO 102
C
C     ******************************************************************
C                                    CALCULATION OF REGRESSION
      SX=0.0
      SY=0.0
      SXY=0.0
      SQX=0.0
      SQY=0.0
```

```
C                                                  R EQUALS R SQUARED
CCCC                                               B EQUALS SLOPE
CCCC                                               SDB EQUALS STANDARD ERROR OF B
C                                                  C EQUALS Y INTERCEPT
                                                   RP EQUALS PROBABILITY VALUE
      IF (MEASUR.EQ.1) GO TO 100
      DO 69 J=1,NENV
   69  Z(J)=AVEE(J)
      ENVAVE=EAVE
  100 CONTINUE
      IF(MEASUR.LT.1) GO TO 101
      ENVAVE=0.6
      DO 76 J=1,NENV
   76 ENVAVE=ENVAVE + Z(J)
      ENVAVE=ENVAVE/NENV
  101 CONTINUE
      DO 75 J=1,NENV
   75 CUM(9)=CUM(9) + (Z(J)-ENVAVE)*(Z(J)-ENVAVE)
      WRITE(6,38)
   38 FORMAT('1',25X,'REGRESSION ANALYSIS',/26X,19('*'),//)
      WRITE(6,39)
   39 FORMAT(1X,'GENOTYPE',6X,'MEAN',6X,'SLOPE',1X,'DIFF TO 1',1X,'SE SL
     1OPE',5X,'Y INTERCEPT',6X,'R SQUARED  ',6X,'PROBABILITY',6X,'HANSON
     2S STABILITY PARAMETER',/1X,131('*'))
      DO 63 I=1,NGEN
      CALL COR(R,B,T,SDB,RP,CUM(1),CUM(2),Z,D,N)
       C=AVEG(I)-(B*ENVAVE)
       T=(1-B)/(SDB/SQRT(ENV))
       T=FISHER(1,NODF(2),T*T)
       WRITE(6,35)I,GNAME(I),AVEG(I),B,T,SDB,C,R,RP,HANSON(I,D,N,AVEG,Z)
   35 FORMAT(1X,I3,1X,A6,1X,F9.4,2X,F9.3,1X,A4,F10.3,6X,F11.3,6X,F11.6,
     *9X,A6,6X,F23.6,/)
       CUM(3)=CUM(3) + B*(AVEG(I)-EAVE)
       CUM(4)=CUM(4) + (AVEG(I)-EAVE)*(AVEG(I)-EAVE)
       CUM(5)=CUM(5) + B
       CUM(6)=CUM(6) +B*B
      CALL COVER(AVEG(I),B,SX,SY,SXY,SQX,SQY)
   63 CONTINUE
C
CCC                                  HETEROGENEITY OF DEVIATION FROM REGRESSION
C     ************************************************************************
      CHI=NODF(2)*((GEN*ALOG(CUM(2)/GEN))-CUM(1))
      CHI=CHI/(1.+(GEN+1.)/3.*GEN*(ENV-1.0))
      PROB=FISHER(NODF(1),10000,CHI/NODF(1))
      WRITE(6,49) ALPHA,CHI,NODF(1),PROB
   49 FORMAT(1X,131('*'),/1X,'ALPHA ',F6.4,/1X,'CHI SQUARE VALUE FOR HET
     *EROGENEITY OF DEVIATION FROM REGRESSION ',F17.3,'   AT ',I4,' DF',
     *6X,'PROBABILITY',4X,A6,//)
      CUM(4)=EAVE-1/(CUM(3)/CUM(4))
      WRITE(6,47)CUM(4)
   47 FORMAT(1X,'POINT OF CONVERGENCE TO X AXIS IS',F15.4,//)
C
CCCC  ************************************************************************
C                                    HETEROGENEITY OF REGRESSIONS CALCULATIONS
                                                  CALCULATION OF ANOVA  VALUES
      CUM(6)=CUM(6)-(CUM(5)*CUM(5))/NGEN
      SS(4)=CUM(6)*CUM(9)
      PROB=SS(4)/SS(3)  * 100.
      WRITE(6,67) PROB
   67 FORMAT(1X,'HETEROGENEITY OF REGRESSION ACCOUNTS FOR 'F6.2,'% OF TH
     *E INTERACTION',//)
      SS(5)=SS(4)*R2COV(SX,SY,SXY,SQX,SQY)
      SS(6)=SS(4)-SS(5)
      SS(7)=SS(3)-SS(4)
  102 NODF(4)=NODF(1)
      NODF(5)=1
      NODF(6)=NODF(1)-1
      NODF(7)=NODF(3)-NODF(1)
      DO 68 I=1,7
      IF(I.GE.1.AND.ISUPP.EQ.10) GO TO 68
      XMS(I)=SS(I)/NODF(I)
      F(I)=XMS(I)/XMS(8)
      P(I)=FISHER(NODF(I),NODF(8),F(I))
   68 CONTINUE
      FF(1)=XMS(1)/XMS(3)
      FF(2)=XMS(2)/XMS(3)
      IF(ISUPP.EQ.10) GO TO 103
      FF(4)=XMS(4)/XMS(7)
      FF(5)=XMS(5)/XMS(6)
      PP(4)=FISHER(NODF(4),NODF(7),FF(4))
      PP(5)=FISHER(NODF(5),NODF(6),FF(5))
  103 PP(1)=FISHER(NODF(1),NODF(3),FF(1))
      PP(2)=FISHER(NODF(2),NODF(3),FF(2))
```

```
C
CCCC  ***********************************************************************
C                                        PARTITION OF VARIANCE CALCULATIONS
                                    GVAR=GENETIC VARIANCE ETC
      GVAR=(XMS(1)-XMS(3))/(ENV*HARMEN)
      GEVAR=(XMS(3)-XMS(8))/HARMEN
      BVAR=(XMS(1)-XMS(7))/(ENV*HARMEN)
      IF(XMS(1).LE.XMS(3)) GVAR=0.0
      IF(XMS(3).LE.XMS(8)) GEVAR=0.0
      IF(BVAR.LT.0.0)BVAR=0.0
      PHVAR=GVAR+GEVAR+XMS(8)
      HB=(GVAR/PHVAR)*100
      CALL SERR(GVAR,PHVAR,XMS(1),XMS(3),XMS(8),NODF(3),NODF(8),SEG,SEP
     *,SEH,SEGE,HARMEN)
      WRITE(6,25)GVAR,SEG
   25 FORMAT(1X,////26X,'PARTITION OF VARIANCE',/26X,21('*'),//1X,'GENET
     *IC VARIANCE',14X,F17.6,4X,'SE=',F20.6,/)
      WRITE(6,26)GEVAR,SEGE,PHVAR,SEP,HB,SEH
   26 FORMAT(1X,'INTERACTION VARIANCE',10X,F17.6,4X,'SE=',F20.6,//1X,'PH
     *ENOTYPIC VARIANCE',11X,F17.6,4X,'SE=',F20.6,//1X,'BROAD SENSE HERI
     *TABILITY',6X,F17.6,'%',3X,'SE=',F20.6,8X,'VALID ONLY IF RANDOM ENV
     *IRONMENTS',/)
      IF(NSUPP.EQ.10) GO TO 107
      HB=(GVAR + BVAR)/PHVAR *100
      WRITE(6,28)BVAR,HB
   28 FORMAT(1X,'REGRESSION VARIANCE ',4X,F23.6,//1X,'HERITABILITY TAKIN
     *G REGRESSION INTO ACCOUNT',F17.2,'%',/)
C
CCC   ***********************************************************************
C                                        ANALYSIS OF VARIANCE TABLE
  107 WRITE(6,41)
   41 FORMAT('1',25X,'ANALYSIS OF VARIANCE',/26X,19('*'),//)
      WRITE(6,18)
   18 FORMAT(8X,'SOURCE OF VARIATION',6X,'DF',4X,'SUM OF SQUARES',4X,'ME
     1AN SQUARE',6X,'VARIANCE RATIO',9X,'PROBABILITY VALUE',/72X,'RANDOM
     2',10X,'FIXED',3X,'RANDOM',10X,'FIXED',/1X,116('*'),/)
      DO 23 I=1,8
      IKE=0
      IF(I.GE.4.AND.I.LE.7) IKE=10
      IF(NSUPP.EQ.10.AND.IKE.EQ.10) GO TO 23
      WRITE(6,19) (ANOVA(I,J),J=1,5),NODF(I),SS(I),XMS(I),FF(I),F(I),PP(
     *I),P(I)
   23 CONTINUE
   19 FORMAT(1X,5A6,I4,F18.4,F15.4,F14.6,F11.6,7X,A6,5X,A6,//)
      WRITE(6,20)
   20 FORMAT(1X,116('*'),//)
      RETURN
      END


C
CCC   THIS SUBROUTINE CONVERTS A NUMBER IN ARRAY IA FROM CHARACTER
CCC   REPRESENTATION TO NUMBER REPRESENTATION
C

      FUNCTION NUMB(IA,S)
      DIMENSION IA(8),NUMBER(80),DREG(10),MDIGIT(10),IDIGIT(10)
      DATA MDIGIT/'0','1','2','3','4','5','6','7','8','9'/
      DATA IDIGIT/0,1,2,3,4,5,6,7,8,9/
      DO 50 J=1,8
   50 NUMBER(J)=-10
      DO 51 I=1,8
      DO 51 J=1,10
   51 IF(IA(I).EQ.MDIGIT(J)) NUMBER(I)=IDIGIT(J)
      K=0
      DO 52 I=1,8
      IF(NUMBER(I).LT.0.AND.K.EQ.0) GO TO 52
      IF(NUMBER(I).GE.0) K=K+1
      IF(NUMBER(I).GE.0) DREG(K)=NUMBER(I)
      IF(NUMBER(I).GE.0) GO TO 52
      NUMB=0
      DO 53 J=1,K
      NUMB=NUMB+DREG(J)*10**(K-J)
      DREG(J)=0
   53 CONTINUE
      K=0
   52 CONTINUE
      RETURN
      END
```

```
C
CCC     SUBROUTINE TO CALCULATE THE STANDARD ERROR OF HERITABILITY
C
        SUBROUTINE SEGER(X,Y,G,GXE,ERR,NGXE,NERR,SG,SP,SEH,SEGE,REP)
C       X = GENETIC VARIANCE :  Y = PHENOTYPIC VARIANCE
        COMMON /A/NGEN/B/NENV
        A=GXE**2/(NGXE+2)
        B=ERR**2/(NERR+2)
        C=A+B+G**2/(NGEN+1)
C       VG =  VARIANCE OF THE GENETIC VARIANCE
        VG=(2.0/((REP*NENV)**2))*C
C               SG,SP =SE OF GENETIC AND PHENOTYPIC VARIANCES
        SG=SQRT(VG)
C       VERP=VARIANCE OF THE WITHIN ENVIRONMENTAL VARIANCE
        VERR=2*B
C       VGXE =VARIANCE OF THE INTERACTION VARIANCE
        VGXE=(2./(REP**2))*(A+B)
        SEGE=SQRT(VGXE)
        VY=VERR*(1.-2./REP-2./(REP*NENV)+2./(REP*REP*NENV))  + VG
      1+ VGXE*(1-2./NENV)
        SP=SQRT(VY)
        COVXY=VG -VERR/REP -VGXE/NENV +(VERR/REP-VERR)/(NENV*REP)
C       COVXY = COVARIANCE BETWEEN X AND Y
        VH=(X**2*VY+Y**2*VG-2*X*Y*COVXY)/(Y**4)
        SEH=SQRT(VH)*100
        RETURN
        END


CCCC    THIS SUBROUTINE PUTS THE NUMBER OF REPLICATES INTO ARRAY N

        SUBROUTINE READN(N)
        COMMON /A/NGEN/B/NENV/G/NGEN1/H/IFILE,IFAST/F/MAXREP
        DIMENSION N(NGEN1,NENV)
        IF(MAXREP.GT.0) GO TO 100
CCCC    READ IN VALUES IF THE NUMBER OF REPLICATES IS UNEQUAL
        IF(IFAST.EQ.1) READ(5,/)((N(I,J),J=1,NENV),I=1,NGEN)
        IF(IFAST.EQ.0) READ(5,/)((N(I,J),I=1,NGEN),J=1,NENV)
        DO 52 I=1,NGEN
        DO 52 J=1,NENV
   52   IF(N(I,J).GT.MAXREP) MAXREP=N(I,J)
        GO TO 200
  100   DO 53 I=1,NGEN
        DO 53 J=1,NENV
   53   N(I,J)=MAXREP
  200   IF(MAXREP.LT.3) MAXREP=3
        RETURN
        END

CCCCC   SUBROUTINE TO CALCULATE THE REGRESSION OF MEANS ON SLOPES
        THIS CAN THEN SHOW WHETHER CONVERGENCE IS AN IMPORTANT PARAMETER

        FUNCTION R2CON(SX,SY,SXY,SQX,SQY)
        COMMON /A/NGEN
        BN=SXY-(SX*SY)/NGEN
        BD=SQX-(SX*SX)/NGEN
        REG=(BN*BN)/BD
        TOT=SQY-(SY*SY)/NGEN
        R2CON=REG/TOT
        RETURN
        END

CCCC    THIS SUBROUTINE ACCUMULATES SUMS OF SQUARES FOR THE CONVERGENCE;

        SUBROUTINE CONVER(X,Y,SX,SY,SXY,SQX,SQY)
        SX=SX  + X
        SY=SY  + Y
        SXY=SXY  + X*Y
        SQX=SQX+X*X
        SQY=SQY+Y*Y
        RETURN
        END
```

```
      FUNCTION FISHER(C,N,X)
C     SUBROUTINE TO CALCULATE PROBALITY THAT F-RATIO GREATER THAN X
CCC   ARGUMENTS : M IS D.F. FOR TREATMENTS, N IS DF FOR ERROR AND X IS
C                                 CALCULATED  F-RATIO
      DIMENSION SIGN(5)
      DATA SIGN/'(NS)',' NS ',' * ',' ** ',' ***'/
      IF(X.LE.1.0) GO TO 110
      INTEGER A,B
      A=2*(M/2)-M+2
      B=2*(N/2)-N+2
      W=X*M/FLOAT(N)
      Z=1.0/(1.0+W)
      IF(A.EQ.1.AND.B.EQ.1) P=SQRT(W)
      IF(A.EQ.1.AND.B.EQ.1) D=0.31830988618 *Z/P
      IF(A.EQ.1.AND.B.EQ.1) P=0.63661977236 *ATAN(P)
      IF(A.EQ.1.AND.B.NE.1) P=SQRT(W*Z)
      IF(A.EQ.1.AND.B.NE.1) D=0.5 * P * Z/W
      IF(A.NE.1.AND.B.EQ.1) P=SQRT(Z)
      IF(A.NE.1.AND.B.EQ.1) D=0.5 * Z * P
      IF(A.NE.1.AND.B.EQ.1) P=1-P
      IF(A.NE.1.AND.B.NE.1) D=Z*Z
      IF(A.NE.1.AND.B.NE.1) P=W*Z
      Y=2.0*W/Z
      IF(A .NE. 1) GO TO 90
      IF( B+2 .GT. N)  GO TO 95
      DO 80 J = B+2,N,2
         D =(J.0 + A/FLOAT(J-2))*D*Z
         P = P +D * Y/(J-1)
   80 CONTINUE
      GO TO 95
   90 ZK = Z**((N-1)/2)
      D  = D * ZK * M/B
      P  = P * ZK + W * Z * (ZK -1)/(Z -1)
   95 Y = W * Z
      Z = 2.0/Z
      B = N -2
      IF( A+2 .GT. M)  GO TO 105
      DO 100  I = A+2,M,2
         J = I + B
         D = Y * D * J/FLOAT(I-2)
         P = P - Z * D/J
  100 CONTINUE
  105 IF( P .GT. 1.0)  P = 1.0
      IF(P .LT. 0.0)  P = 0.0
      T=1.0 - P
       IF(T.GT.0.10) KUM=2
       IF(T.LE.0.10.AND.T.GT.0.05) KUM=1
       IF(T.LE.0.05.AND.T.GT.0.01) KUM=3
       IF(T.LE.0.01.AND.T.GT.0.001) KUM=4
       IF(T.LE.0.001) KUM=5
      FISHER=SIGN(KUM)
      RETURN
  110 FISHER=SIGN(2)
      RETURN
      END


CCCCC
      THIS FUNCTION CALCULATES HANSONS STABILITY PARAMETER
      A COMPARATIVE MEASURE COMPARED TO AN IDEAL STABLE GENOTYPE
      WITH A SLOPE OF (1 - ALPHA)

      FUNCTION HANSON(I,D,N,AVEG,Z)
      COMMON /A/NGEN/B/NENV/C/MEAN/D/ENVAVE/E/ALPHA/F/MAXREP/G/JGEN1
      DIMENSION D(MAXREP,NGEN,NENV),N(NGEN1,NENV),AVEG(NGEN),Z(NENV)
      GEN=NGEN
      ENV=NENV
      QA=0.0
      DO 10 J=1,NENV
        QA=QA + (D(KMEAN,I,J)-AVEG(I)-(Z(J) -ENVAVE)*ALPHA)**2
   10 CONTINUE
      IF(QA.GT.0.0) HANSON=SQRT(QA)
      IF(QA.LE.0.0) HANSON=0.0
      RETURN
      END
```

```
C
C
C     THIS SUBROUTINE TRANSFORMS THE DATA
C     TRANSFORMATION CODE
C  1=SQUARE ROOT;2=LOG E; 3=LOG 10; 4=1/(1+X); 5=ARCSINE; 6=ARCSINE/100

      SUBROUTINE TRANSF(NTRAN,D,N)
      COMMON /A/NGEN/B/NENV/F/MAXREP/G/NGEN1
      DIMENSION D(MAXREP,NGEN,NENV),N(NGEN1,NENV)
      IF(NTRAN.LE.0) GO TO 4
      DO 1 I=1,NGEN
       DO 2 J=1,NENV
        IF(N(I,J).LE.0) GO TO 10
        DO 3 K=1,N(I,J)
         IF(NTRAN.EQ.1)                    D(K,I,J)=SQRT(D(K,I,J)+1)
         IF(NTRAN.EQ.2)                    D(K,I,J)=ALOG(D(K,I,J)+1)
         IF(NTRAN.EQ.3)                    D(K,I,J)=ALOG10(D(K,I,J)+1)
         IF(NTRAN.EQ.4)                    D(K,I,J)=1./(1.+D(K,I,J))
         IF(NTRAN.EQ.5) D(K,I,J)=(ARSIN(D(K,I,J)))/0.01745329
         IF(NTRAN.EQ.6) D(K,I,J)=(ARSIN(D(K,I,J)/100))/0.01745329
    3   CONTINUE
    2  CONTINUE
    1  CONTINUE
       IF(NTRAN.EQ.1) WRITE(6,12)
       IF(NTRAN.EQ.2) WRITE(6,13)
       IF(NTRAN.EQ.3) WRITE(6,14)
       IF(NTRAN.EQ.4) WRITE(6,15)
       IF(NTRAN.EQ.5) WRITE(6,16)
       IF(NTRAN.EQ.6) WRITE(6,17)
   12  FORMAT(31X,'DATA IS TRANSFORMED BY SQRT(X+1)',/)
   13  FORMAT(31X,'DATA IS TRANSFORMED BY LOG E (X+1)',/)
   14  FORMAT(31X,'DATA IS TRANSFORMED BY LOG 10 (X+1)',/)
   15  FORMAT(31X,'DATA IS TRANSFORMED BY 1/(1+X)',/)
   16  FORMAT(31X,'DATA IS TRANSFORMED BY ARCSINE X',/)
   17  FORMAT(31X,'DATA IS TRANSFORMED BY ARCSINE (X/100)',/)
       RETURN
   10  WRITE(6,20)
   20  FORMAT(1X//1X,'THE NUMBER OF REPLICATES CAN NOT EQUAL ZERO IN THIS
     * ANALYSIS,MUST BE AT LEAST ONE REPLICATE')
       STOP
       END


C
C     THIS SUBROUTINE DOES THE REGRESSION ANALYSIS

      SUBROUTINE COR(R,B,I,SDB,BP,SUM,SSQ,AVEE,D,N)
      COMMON /A/NGEN/B/NENV/G/NGEN1/C/NMEAN/F/MAXREP
      DIMENSION AVEE(NENV),D(MAXREP,NGEN,NENV),N(NGEN1,NENV)
      SX=0.0
      SY=0.0
      SQX=0.0
      SQY=0.0
      SXY=0.0
      DO 100 J=1,NENV
       Y=D(NMEAN,I,J)
       X=AVEE(J)
       SX=SX+X
       SY=SY+Y
       SXY=SXY+(X*Y)
      SQX=SQX+X*X
      SQY=SQY+Y*Y
  100 CONTINUE
      BN=(SXY-((SX*SY)/NENV))
      BD=(SQX-((SX**2)/NENV))
      REG=(BP*BD)/BD
      B=BN/BD
      TOT=SQY-(SY*SY)/NENV
      IF(REG/TOT.GE.0.0) R=REG/TOT
      IF(REG/TOT.LT.0.0) R=0.0
      IF(B.LT.0.0) R=-R
      DEV=TOT-REG
      MDLVDF=NENV-2
      DEVMS=DEV/MDLVDF
      SDB=DEVMS/(SQX-((SX*SX)/NENV))
      IF(SDB.GT.0.0) SDB=SQRT(SDB)
      IF(SDB.LE.0.0) SDB=0.0
      IF(DEVMS.GT.0.0) VR=REG/DEVMS
      IF(DEVMS.LE.0.0) VR=-1
      BP=FISHER(1,MDLVDF,VR)
      SUM=SUM + ABS(DEVMS)
      SSQ=SSQ + DEVMS
      RETURN
      END
```

```
C
C     THIS SUBROUTINE READS IN THE DATA
C     OFF FILE OR CARDS, COLUMN , FIXED OR FREE FORMAT
C
      SUBROUTINE READE(IFORM,D,N)
      COMMON /A/NGEN/B/NENV/F/MAXREP/G/NGEN1/H/NREAD/J/NUSE/M/IFILE,IFAS
     *T/N/INPUT
      DIMENSION N(NGEN1,NENV),D(MAXREP,NGEN,NENV),IFORM(74),VARY(80)
      IF(IFILE.GT.0) WRITE(6,203)
  203 FORMAT(1X,'THE DATA IS READ FROM FILE NUMBER 3')
      IF(INPUT.LT.3) GO TO 52
      IF(IFAST.EQ.1) GO TO 51
C
C     GENOTYPES ITERATE THE FASTEST
C
      DO 50 J=1,NENV
      DO 50 I=1,NGEN
      DO 50 K=1,N(I,J)
      IF(IFILE.EQ.0) READ(5,IFORM) (VARY(L),L=1,NREAD)
      IF(IFILE.GE.1) READ(IFILE) (VARY(L),L=1,NREAD)
      D(K,I,J)=VARY(NUSE)
   50 CONTINUE
   51 IF(IFAST.EQ.0) GO TO 52
      DO 53 I=1,NGEN
      DO 53 J=1,NENV
      DO 53 K=1,N(I,J)
      IF(IFILE.EQ.0) READ(5,IFORM) (VARY(L),L=1,NREAD)
      IF(IFILE.GE.1) READ(IFILE) (VARY(L),L=1,NREAD)
      D(K,I,J)=VARY(NUSE)
   53 CONTINUE
   52 CONTINUE
      IF(INPUT.EQ.3) GO TO 100
      IF(IFAST.EQ.1) GO TO 54
      IF(IFILE.EQ.0.AND.INPUT.EQ.1) READ(5,/)(((D(K,I,J),K=1,N(I,J)),
     *I=1,NGEN),J=1,NENV)
      IF(IFILE.EQ.0.AND.INPUT.EQ.2)READ(5,IFORM)(((D(K,I,J),K=1,N(I,J)),
     *I=1,NGEN),J=1,NENV)
      IF(IFILE.GE.1) READ(IFILE)(((D(K,I,J),K=1,N(I,J)),I=1,NGEN),J=1,NE
     *NV)
   54 IF(IFAST.EQ.0) GO TO 56
C
C     ENVIRONMENTS ITERATE THE FASTEST
C
      IF(IFILE.EQ.0.AND.INPUT.EQ.2)READ(5,IFORM)(((D(K,I,J),K=1,N(I,J)),
     *J=1,NENV),I=1,NGEN)
      IF(IFILE.EQ.0.AND.INPUT.EQ.1)READ(5,/)(((D(K,I,J),K=1,N(I,J)),
     *J=1,NENV),I=1,NGEN)
      IF(IFILE.GE.1) READ(IFILE)(((D(K,I,J),K=1,N(I,J)),J=1,NENV),I=1,NG
     *EN)
   56 CONTINUE
  100 RETURN
      END
```

TITLE RHIZOME LENGTHS OF THE SIX T.AMBIGUUM POPULATIONS AT FIVE ENVIRONMENTS
****

THE NUMBER OF ENVIRONMENTS EQUALS 5
THE NUMBER OF GENOTYPES EQUALS 6
ALPHA = 0.800
THE DATA IS READ FROM FILE NUMBER 3

HOMOGENEITY OF VARIANCE (BARTLETS TEST)
****

DF 29 CHI SQUARE 489.221 PROBABILITY ***

ENVIRONMENTAL MEANS
****

MEAN OF ENVIRONMENT 1(WAK/LO) IS	27.252462	SE OF GENOTYPE MEANS =	6.980642
MEAN OF ENVIRONMENT 2(CAS/LO) IS	34.032006	SE OF GENOTYPE MEANS =	8.302458
MEAN OF ENVIRONMENT 3(WAK/MD) IS	10.775776	SE OF GENOTYPE MEANS =	3.040164
MEAN OF ENVIRONMENT 4(CAS/MD) IS	21.973931	SE OF GENOTYPE MEANS =	4.816971
MEAN OF ENVIRONMENT 5(SPE/HI) IS	14.625442	SE OF GENOTYPE MEANS =	3.411966
GRAND MEAN	21.731924		
COEFFICIENT OF VARIATION	53.49%		

DO THE ENVIRONMENTS HAVE DIFFERENT ERROR VARIANCES
CHI SQUARE 461.188 AT 4 DF PROBABILITY ***

REGRESSION ANALYSIS

GENOTYPE	MEAN	SLOPE	DIFF TO 1	SE SLOPE	Y INTERCEPT	R SQUARED	PROBABILITY	HANSONS STABILITY PARAMETER
1 FOREST	21.0793	0.648	***	0.082	6.990	0.954396	**	3.896521
2 SUMMIT	13.9079	0.589	***	0.087	1.108	0.938801	**	4.863941
3 51140	21.6094	1.113	NS	0.166	-2.568	0.937507	**	7.968307
4 TRELIN	20.7690	1.026	NS	0.080	-1.520	0.981943	**	4.975696
5 57353	25.1018	1.388	***	0.088	-5.060	0.988010	***	11.402557
6 PRAIRY	27.9241	1.237	**	0.085	1.050	0.986064	***	8.647743

ALPHA 0.8000
CHI SQUARE VALUE FOR HETEROGENEITY OF DEVIATION FROM REGRESSION 0.070 AT 5 DF PROBABILITY NS

POINT OF CONVERGENCE TO X AXIS IS 3.5602

HETEROGENEITY OF REGRESSION ACCOUNTS FOR 1.39% OF THE INTERACTION

PARTITION OF VARIANCE

GENETIC VARIANCE	19.983192	SE=	12.026635	
INTERACTION VARIANCE	9.790488	SE=	3.729711	
PHENOTYPIC VARIANCE	164.877878	SE=	18.086211	
BROAD SENSE HERITABILITY	12.119996%	SE=	7.422702	VALID ONLY IF RANDOM ENVIRONMENTS
REGRESSION VARIANCE	0.000000			

HERITABILITY TAKING REGRESSION INTO ACCOUNT 12.12%

ANALYSIS OF VARIANCE

SOURCE OF VARIATION	DF	SUM OF SQUARES	MEAN SQUARE	VARIANCE RATIO RANDOM	VARIANCE RATIO FIXED	PROBABILITY VALUE RANDOM	PROBABILITY VALUE FIXED
GENOTYPES	5	29446.5713	5889.3143	9.079693	43.590905	***	***
ENVIRONMENTS	4	110891.6958	27722.9240	42.741077	205.196615	***	***
INTERACTION (G X E)	20	12972.4966	648.6248	0.000000	4.800923		***
HETEROGENEITY OF REGRESSIONS	5	180.5384	36.1077	0.042340	0.267258	NS	NS
CONVERGENCE	1	119.8156	119.8156	7.892618	0.886838	*	NS
NONCONVERGENCE	4	60.7228	15.1807	0.000000	0.112363		NS
RESIDUAL	15	12791.9582	852.7972	0.000000	6.312144		***
ERROR BETWEEN REPLICATES	1574	212654.0062	135.1042	0.000000	0.000000		

GENCOR

A program written to calculate phenotypic and genotypic correlations between variates measured in genotype environment interaction experiments (n genotypes completely randomised in m environments).

Prints Out:

F ratio from analysis of variance of each variate, correlation matrix, phenotypic and genotypic. (calculated according to statistical materials and methods).

Mean squares for analysis of covariance and variance of all characteristics.

SE of correlation coefficients, after Tallis (1959), Robertson (1959) and Scheinberg (1966).

N.B. To accommodate a particular experimental design the dimensions of the "D" (data) array, "W" (data for anova) array and "N" (replicates) array may have to be changed.

Instructions for use of GENCOR

Explaining necessary cards and functions of each.

TITLE ... includes any title, written out, optional

GENOTYPES n number of genotypes

ENVIRONMENTS m number of environments

The order of these 2 cards is important, control which iterates the fastest for reading in of unequal replicates and data. First iterates the slowest.

REPLICATES = ℓ * where ℓ is the number of replicates. If unequal the number of replicates is read in starting on the next card, free format separated by commers.

READ k where k equals the number of variates to be read in

DELETE i where i is the number of variates read in which are to be deleted from analysis. Next card contains 1's in the column of variate to be deleted e.g.: 1 in column 13 deletes variate 13 from analysis. This card is optional.

NAMES This card is essential and is followed by variate names on next card 10A6 format.

FREE reads from free format, separated by commers.

FIXED reads from fixed format, format given below.

COLUMN reads from column format, format given below. One of the above three cards is essential.

FORMAT followed by format of data.

FILE reads binary data from file 3.

TRANSFORM j where j is integer from 0 to 6.

0 = raw data 1 = square root (x+1) 2 = $\log_e$ (x+1) 3 = $\log_{10}$ (x+1) 4 = 1/(x+1) 5 = arcsine (x) 6 = arcsine (x/100)

* presence of equals sign signifies equal replicates

PRINT	prints out SE of correlation matrix and mean square matrix, optional.
DATA	followed by data deck.

```
C GENOTYPIC CORRELATIONS FROM GENOTYPE X ENVIRONMENT ANALYSIS
C
C     READS TITLE CARD, GENOTYPE CARD,ENVIRONMENT CARD AND REPLICATES
C
FILE  3(TITLE="MYSELF.",KIND=DISK)

      DIMENSION TOTAL(171 ,40),TOT(170),SIGN(40,40),SIG(40,40),W(170,2
     *5,5),GCOV(40,40),SECOR(40,40),GX(40),GR(40),XR(40),NTRAN(40),N(170
     *,25),ZMSG(40,40),ZMSR(40,40),ZMSX(40,40),PHENR(40,40),AN(40),
     *D(165,5,2,38)
      COMMON /C/NENV/F/NGEN/Z/NGEN1
      DIMENSION IB(74)
      NREP=0
  100 A="      "
      DO 50 I=1,74
   50 IB(I)=" "
      READ(5,1)A,(IB(I),I=1,74)

    1 FORMAT(A6,74A1)
      IF(A.IS."TITLE ") WRITE(6,2) A,(IB(I),I=1,74)

    2 FORMAT('1',25X,A6,74A1,/26X,80('*'),//)
      IF(A.IS."TITLE ") GO TO 100
      IF(A.IS."GENOTY") NGEN=NUMB(IB,74)
      IF(A.IS."GENOTY") IFAST=0
      IF(A.IS."GENOTY") GO TO 100
      IF(A.IS."ENVIRO") NENV=NUMB(IB,74)
      IF(A.IS."ENVIRO") IFAST=1
      IF(A.IS."ENVIRO") GO TO 100
      IF(A.IS."REPLIC") GO TO 10
      GO TO 30
   10 DO 51 J=1,74
   51 IF(IB(J).IS."=") NREP=NUMB(IB,74)
      WRITE(6,3)NGEN,NENV
    3 FORMAT(1X,'NUMBER OF GENOTYPES = ',I6,/1X,'NUMBER OF ENVIRONMENTS
     *= ',I6)
      IF(NREP.GT.0) WRITE(6,4) NREP
    4 FORMAT(1X,'ALL REPLICATES ARE OF EQUAL SIZE; NUMBER = 'I6)
      IF(NREP.EQ.0) WRITE(6,5)
    5 FORMAT(1X,'THERE IS AN UNEQUAL NUMBER OF REPLICATES')
      IF(IFAST.EQ.0) WRITE(6,6)
    6 FORMAT(1X,'FOR READING CARDS; GENOTYPES ITERATE FASTER THAN ENVIRO
     *NMENTS')
      IF(IFAST.EQ.1) WRITE(6,7)
    7 FORMAT(1X,'FOR READING CARDS; ENVIRONMENTS ITERATE FASTER THAN GEN
     *OTYPES')
      IF(NGEN.LE.1.OR.NENV.LE.1) STOP
      NGEN1=NGEN+1
      CALL ONE(IFAST,NREP,D,N,NTRAN,AN)
C
C     CALLS THE MAIN PROGRAM, ONCE INPUT OPTIONS ARE SORTED OUT
C
      CALL ACTION(TOTAL,TOT,SIGN,SIG,W,GCOV,SECOR,GX,GR,XR,NTRAN,N,ZMSG,
     *ZMSX,ZMSR,PHENR,AN,D)
      STOP
   30 WRITE(6,8)
    8 FORMAT(1X,'NO REPLICATES CARD WAS PRESENT')
      STOP
      END
C
C     CALCULATES PHENOTYPIC VARIANCE
C
      FUNCTION VP(I,J,XMSG)
      COMMON /B/NVAR/E/NGDF
      DIMENSION XMSG(NVAR,NVAR)
      VP=(XMSG(I,I)*XMSG(J,J)+XMSG(I,J)*XMSG(I,J))/(NGDF+2)
      RETURN
      END
```

```
      SUBROUTINE ACTION(TOTAL,TOT,SIGN,SIG,A,GCOV,SECOR,GX,GR,XR,NTR,N,Z
     1MSG,ZMSX,ZMSR,PHENR,AN,D)
      COMMON /B/NVAR/C/NENV/F/NGEN/L/MAXREP/K/HARMEN/E/NGDF/H/NXDF,NRDF
     */Z/NGEN1/O/NSUP
      DIMENSION TOTAL(NGEN1  ,NVAR),TOT(NGEN),SIGN(NVAR,NVAR),SIG(NVAR,NV
     1AR),A(NGEN,NENV,MAXREP),GCOV(NVAR,NVAR),SECOR(NVAR,NVAR),GX(NVAR),
     2GR(NVAR),XR(NVAR),NTR(NVAR),N(NGEN,NENV),ZMSG(NVAR,NVAR),ZMSR(NVAR
     3,NVAR),ZMSX(NVAR,NVAR),PHENR(NVAR,NVAR),AN(NVAR),D(NGEN,NENV,MAXRE
     4P,NVAR)
C
C     PLACE SINGLE VARIATE IN ARRAY A FOR ANOVA SUBROUTINE
C
      DO 1 L=1,NVAR
C
C     TRANSFORM THE VARIATE BEFORE ANALYSIS
C
      CALL TRANSF(NTR(L),D,N,L)
        DO 2 I=1,NGEN
          DO 3 J=1,NENV
            DO 4 K=1,N(I,J)
              A(I,J,K)=D(I,J,K,L)
4           CONTINUE
3         CONTINUE
2       CONTINUE
C
C     CALL ANOVA SUBROUTINE TO CALCULATE DIAGONAL VALUES: VARIANCE
C
      CALL ANOVA(A,NGDF,NEDF,NXDF,NRDF,GMS,EMS,XMS,RMS,TOT,EAVE,N)
C
C     PLACE THE MEAN SQUARES INTO APPROPRIATE ARRAY
C     ZMSG=GENOTYPIC; ZMSX=INTERACTION; ZMSR=ERROR:
C
        ZMSG(L,L)=GMS
        ZMSX(L,L)=XMS
        ZMSR(L,L)=RMS
        DO 5 I=1,NGEN
          TOTAL(I,L)=TOT(I)
5       CONTINUE
        TOTAL(NGEN+1,L)=EAVE
C
C      CALCULATE THE GENETIC VARIANCE , PLACE IN GCOV
C
        IF(ZMSG(L,L).GT.ZMSX(L,L).AND.ZMSX(L,L).GT.ZMSR(L,L))
     *  GCOV(L,L)=(ZMSG(L,L)-ZMSX(L,L))/NGEN
        IF(ZMSG(L,L).GT.ZMSR(L,L).AND.ZMSX(L,L).LE.ZMSR(L,L))
     *  GCOV(L,L)=(ZMSG(L,L)-((ZMSX(L,L)*NXDF+ZMSR(L,L)*NRDF)/
     *  (NRDF+NXDF)))/NGEN
        IF(ZMSG(L,L).LE.ZMSR(L,L)) GCOV(L,L)=0.0
1     CONTINUE
C
C     PLACE SUM OF 2 VARIATES IN A FOR ANOVA TO CALCULATE COVARIANCE
C
      DO 6 L1=1,NVAR-1
        DO 7 L2=L1+1,NVAR
          DO 8 I=1,NGEN
            DO 9 J=1,NENV
              DO 10 K=1,N(I,J)
                A(I,J,K)=D(I,J,K,L1)+D(I,J,K,L2)
10            CONTINUE
9           CONTINUE
C
C     SSQ IS USED TO CALCULATE SIGN OF CORRELATION ;SIGN IS USED FOR THIS
C
            SSQ=SSQ+TOTAL(I,L1)*TOTAL(I,L2)
8         CONTINUE
C
C     CALL ANOVA TO CALCULATE COVARIANCE COMPONENTS
C
          CALL ANOVA(A,NGDF,NEDF,NXDF,NRDF,GMS,EMS,XMS,RMS,TOT,EAVE,N)
          ZMSG(L1,L2)=ABS(GMS-ZMSG(L1,L1)-ZMSG(L2,L2))/2.
          ZMSX(L1,L2)=ABS(XMS-ZMSX(L1,L1)-ZMSX(L2,L2))/2.
          ZMSR(L1,L2)=ABS(RMS-ZMSR(L1,L1)-ZMSR(L2,L2))/2.
          SIGN(L1,L2)=SSQ-(TOTAL(NGEN+1,L1)*TOTAL(NGEN+1,L2))/NGEN
          SSQ=0.0
C
C     GENETIC COVARIANCES ARE CALCULATED
C
          IF(ZMSG(L1,L2).GT.ZMSX(L1,L2).AND.ZMSX(L1,L2).GT.ZMSR(L1,L2))
     *    GCOV(L1,L2)=(ZMSG(L1,L2)-ZMSX(L1,L2))/NGEN
          IF(ZMSG(L1,L2).GT.ZMSR(L1,L2).AND.ZMSX(L1,L2).LE.ZMSR(L1,L2))
     *    GCOV(L1,L2)=(ZMSG(L1,L2)-((ZMSX(L1,L2)*NXDF+ZMSR(L1,L2)*NRDF)/
     *    (NRDF+NXDF)))/NGEN
```

```
          IF(ZMSG(L1,L2).LE.ZMSR(L1,L2)) GCOV(L1,L2)=0.0
C
C     CALCULATE GENOTYPIC CORRELATIONS ; PLACE IN LOWER HALF OF PHENR
C
          IF(GCOV(L1,L1)*GCOV(L2,L2).GT.0.0)
         *     PHENR(L2,L1)=GCOV(L1,L2)/(SQRT(GCOV(L1,L1)*GCOV(L2,L2)))
          IF(GCOV(L1,L1)*GCOV(L2,L2).LE.0.0)PHENR(L2,L1)=0.0
C
C     CALCULATE PHENOTYPIC CORRELATIONS; PLACE IN TOP HALF OF PHENR
C
          IF(ZMSG(L1,L1)*ZMSG(L2,L2).GT.0.0)
         *     PHENR(L1,L2)=ZMSG(L1,L2)/(SQRT(ZMSG(L1,L1)*ZMSG(L2,L2)))
          IF(ZMSG(L1,L1)*ZMSG(L2,L2).LE.0.0)PHENR(L1,L2)=0.0
          IF(SIGN(L1,L2).LT.0.0)PHENR(L2,L1)=-PHENR(L2,L1)
          IF(SIGN(L1,L2).LT.0.0) PHENR(L1,L2)=-PHENR(L1,L2)
    7   CONTINUE
    6 CONTINUE
C
C     DIAGONAL CORRELATIONS EQUAL 1
C
        DO 11 L=1,NVAR
          PHENR(L,L)=1.0
C
C     F RATIOS OF THE ANALYSIS OF VARIANCE ARE CALCULATED
C     GX=G TESTED AGAINST INTERACTION; GR=G TESTED AGAINST ERROR;
C      XR=INTERACTION TESTED AGAINST ERROR
C
        IF(ZMSX(L,L).GT.0.0) GX(L)=ZMSG(L,L)/ZMSX(L,L)
        IF(ZMSR(L,L).GT.0.0) GR(L)=ZMSG(L,L)/ZMSR(L,L)
        IF(ZMSR(L,L).GT.0.0) XR(L)=ZMSX(L,L)/ZMSR(L,L)
        IF(ZMSX(L,L).LE.0.0) GX(L)=0.0
        IF(ZMSR(L,L).LE.0.0) XR(L)=0.0
        IF(ZMSR(L,L).LE.0.0) GR(L)=0.0
   11 CONTINUE
C
C     WRITE CORRELATION MATRIX
C
        WRITE(6,19)
   19 FORMAT(1X,//1X,'CORRELATION MATRIX; PHENOTYPIC ABOVE DIAGONAL, GEN
      *OTYPIC BELOW',/1X,62('*'))
        WRITE(6,17)(AN(J),J=1,NVAR)
   17 FORMAT(1X,//1X,12X,12(2X,A6,2X))
        NAST=NVAR*10
        IF(NAST.GT.120) NAST=120
        WRITE(6,33) NAST
   33 FORMAT(1X,12('*'),*('*'))
        WRITE(6,25)(GX(J),J=1,NVAR)
   25 FORMAT(1X,'G/X',9X,12(F8.2,2X))
        WRITE(6,24)(GR(J),J=1,NVAR)
   24 FORMAT(1X,'G/ERROR',5X,12(F8.2,2X))
        WRITE(6,26)(XR(J),J=1,NVAR)
   26 FORMAT(1X,'X/ERROR',5X,12(F8.2,2X))
        WRITE(6,33) NAST
        DO 20 I=1,NVAR
   20   WRITE(6,13)AN(I),(PHENR(I,J),J=1,NVAR)
   13 FORMAT('0',2X,A6,2X,12(2X,F8.4))
C
C     WRITE MEAN SQUARE ARRAYS IF NSUP = 1
C
        IF(NSUP.EQ.0) GO TO 123
        WRITE(6,124)
  124 FORMAT('1','MEAN SQUARE ARRAY FOR GENOTYPES, INTERACTION AND ERROR
      * RESPECTIVELY',/1X,67('*')//)
        WRITE(6,17)(AN(J),J=1,NVAR)
        WRITE(6,33) NAST
        DO 126 I=1,NVAR
        WRITE(6,125)AN(I),(ZMSG(I,J),J=1,NVAR)
        WRITE(6,125)AN(I),(ZMSX(I,J),J=1,NVAR)
        WRITE(6,125)AN(I),(ZMSR(I,J),J=1,NVAR)
  125 FORMAT(1X,2X,A6,2X,12(F10.3))
        WRITE(6,33) NAST
  126 CONTINUE
  123 CONTINUE
C
C     SEOFR IS A SUBROUTINE TO CALCULATE THE STANDARD ERROR OF CORRELATIONS
C
        CALL SEOFR(ZMSG,ZMSX,ZMSR,PHENR,GCOV,AN,SECOR,SIG)
  999 STOP
        END
```

```
C
C     THIS SUBROUTINE CALCULATES THE STANDARD ERRORS OF THE CORRELATIONS
C
      SUBROUTINE SECOR(XMSG,XMSX,XMSR,PHENR,GCOV,AN,SECOR,SIG)
      COMMON /B/NVAR/F/NGEN/O/NSUP
      DIMENSION SECOR(NVAR,NVAR),SIG(NVAR,NVAR),ZA(5),XMSG(NVAR,NVAR),
     1PHENR(NVAR,NVAR),GCOV(NVAR,NVAR),AN(NVAR),XMSX(NVAR,NVAR),XMSR(NVA
     2R,NVAR)
      DATA ZA/'***','**','*','(NS)','NS'/
      DO 12 I=1,NVAR
   12 SECOR(I,I)=0.0
C
C     CALCULATE THE SE FOR PHENOTYPIC CORRELATIONS
C     SE ARE PUT INTO ARRAY SECOR, ABOVE THE DIAGONAL
C
      DO 10 I=1,NVAR-1
      DO 10 J=I+1,NVAR
      NUT=0
      IF(XMSG(I,J).LE.0.0.OR.XMSG(I,I).LE.0.0) NUT=1
      IF(XMSG(J,J).LE.0.0.OR.NUT.EQ.1) GO TO 20
      IF(PHENR(I,J).EQ.0.0) GO TO 20
      VARP=PHENR(I,J)*PHENR(I,J)*(VP(I,J,XMSG)/(XMSG(I,J)*XMSG(I,J)) +
     1VP(I,I,XMSG)/(4*XMSG(I,I)*XMSG(I,I)) + VP(J,J,XMSG)/(4*XMSG(J,J) *
     2XMSG(J,J)) - COVP(I,J,I,I,XMSG)/(XMSG(I,J)*XMSG(I,I)) -
     3COVP(I,J,J,J,XMSG)/(XMSG(I,J)*XMSG(J,J))    -
     4 COVP(I,I,J,J,XMSG)/(2*XMSG(I,I)*XMSG(J,J)))
      IF(VARP.GT.0.0) SECOR(I,J)=SQRT(VARP)
      IF(VARP.LE.0.0) SECOR(I,J)=0.0
      GO TO 15
   20 SECOR(I,J)=0.0
C
C     CALCULATE THE SE FOR GENOTYPIC CORRELATIONS
C     SE ARE PUT INTO ARRAY SECOR, BELOW THE DIAGONAL
C
   15 NUT=0
      IF(GCOV(I,J).LE.0.0.OR.GCOV(I,I).LE.0.0) NUT=1
      IF(GCOV(J,J).LE.0.0.OR.NUT.EQ.1) GO TO 30
      IF(PHENR(J,I).EQ.0.0) GO TO 30
      VARG=PHENR(J,I)*PHENR(J,I) *
     1(  VG(I,J,XMSG,XMSX,XMSR)/ (GCOV(I,J)*GCOV(I,J) )  +
     2VG(I,I,XMSG,XMSX,XMSR)/(4*GCOV(I,I)*GCOV(I,I))
     3+ VG(J,J,XMSG,XMSX,XMSR)/(4*GCOV(J,J)*GCOV(J,J))   -
     4COVG(I,J,I,I,XMSG,XMSX,XMSR)/(GCOV(I,J)*GCOV(I,I)) -
     5COVG(I,J,J,J,XMSG,XMSX,XMSR)/(GCOV(I,J)*GCOV(J,J)) +
     6COVG(I,I,J,J,XMSG,XMSX,XMSR)/(2*GCOV(I,I)*GCOV(J,J)))
      IF(VARG.LE.0.0) SECOR(J,I)=0.0
      IF(VARG.GT.0.0)SECOR(J,I)=SQRT(VARG)
      GO TO 25
   30 SECOR(J,I)=0.0
   25 CONTINUE
   10 CONTINUE
C
C     SE MATRIX IS WRITTEN OUT IF A : PRINT : CARD IS USED
C
      NAST=NVAR*10
      IF(NAST.GT.120) NAST=120
      IF(NSUP.EQ.0) GO TO 83
      WRITE(6,50)
   50 FORMAT('1','SE OF CORRELATION MATRIX',/1X,24('*')//)
      WRITE(6,51)(AN(J),J=1,NVAR)
   51 FORMAT(1X,12X,12(2X,A6,2X))
      WRITE(6,33) NAST
   33 FORMAT(1X,12('*'),*('*'))
      DO 52 I=1,NVAR
   52 WRITE(6,53)AN(I),(SECOR(I,J),J=1,NVAR)
   53 FORMAT('0',2X,A6,2X,12(2X,F8.4))
   83 CONTINUE
C
C     A T TEST IS DONE TO DETERMINE IF THE CORRELATIONS ARE SIGNIFICANT
C
      DO 21 I=1,NVAR
        DO 22 J=1,NVAR
      IF(PHENR(I,J).GT.1.0) PHENR(I,J)=1.0
      IF(PHENR(I,J).LT.-1.0) PHENR(I,J)=-1.0
      IF(SECOR(I,J).GT.0.00000001) T=PHENR(I,J)/SECOR(I,J)
      IF(SECOR(I,J).LE.0.00000001) T=0.0
          P=FISHER(1,NGEN-2,T*T)
          IF(P.GT.0.100) SIG(I,J)=ZA(5)
          IF(P.LE.0.100) SIG(I,J)=ZA(4)
          IF(P.LE.0.050) SIG(I,J)=ZA(3)
          IF(P.LE.0.010) SIG(I,J)=ZA(2)
          IF(P.LE.0.001) SIG(I,J)=ZA(1)
```

```
   22   CONTINUE
   21 CONTINUE
C
CCC
      THE SIGNIFICANCE MATRIX IS THEN WRITTEN OUT
C
      WRITE(6,54)
   54 FORMAT('1','SIGNIFICANCE OF CORRELATION MATRIX; BY THE T TEST',/1X
     *,49('*')//)
      WRITE(6,51) (AN(J),J=1,NVAR)
      WRITE(6,33) NAST
      DO 55 I=1,NVAR
   55 WRITE(6,56) AN(I),(SIG(I,J),J=1,NVAR)
   56 FORMAT('0',2X,A6,2X,12(4X,A6))
      RETURN
      END

C
CCC
      READS DATA OFF CARDS OR FILES, FREE, FIXED OR COLUMN FORMAT

      SUBROUTINE READE(N,D,IFO,IFILE,IFAST,NVARED,INPUT,IVO,NX)
      COMMON /B/NVAR/F/NGEN/C/NENV/L/MAXREP
      DIMENSION N(NGEN,NENV),D(NGEN,NENV,MAXREP,NVAR),IFO(74)
      DIMENSION VARY(73),NX(80)
      IF(INPUT.LT.3) GO TO 52
      IF(IFAST.EQ.1) GO TO 51
      DO 50 J=1,NENV
      DO 50 I=1,NGEN
      DO 50 K=1,N(I,J)
      IF(IFILE.EQ.0) READ(5,IFO) (VARY(L),L=1,NVARED)
      IF(IFILE.EQ.1) READ(IVO) (VARY(L),L=1,NVARED)
      KK=1
      L=1
   10 IF(NX(L).EQ.0) D(I,J,K,KK)=VARY(L)
      IF(NX(L).LE.0) KK=KK+1
      L=L+1
      IF(KK.LE.NVAR) GO TO 10
   50 CONTINUE
   51 IF(IFAST.EQ.0) GO TO 52
      DO 53 I=1,NGEN
      DO 53 J=1,NENV
      DO 53 K=1,N(I,J)
      IF(IFILE.EQ.0) READ(5,IFO) (VARY(L),L=1,NVARED)
      IF(IFILE.EQ.1) READ(IVO) (VARY(L),L=1,NVARED)
      KK=1
      L=1
   20 IF(NX(L).EQ.0) D(I,J,K,KK)=VARY(L)
      IF(NX(L).LE.0) KK=KK+1
      L=L+1
      IF(KK.LE.NVAR) GO TO 20
   53 CONTINUE
   52 CONTINUE
      IF(INPUT.EQ.3) GO TO 56
      IF(IFAST.EQ.1) GO TO 54
      DO 55 L=1,NVARED
      IF(IFILE.EQ.0.AND.INPUT.EQ.1) READ(5,/)(((D(I,J,K,L),K=1,N(I,J)),
     *I=1,NGEN),J=1,NENV)
      IF(IFILE.EQ.0.AND.INPUT.EQ.2)READ(5,IFO)(((D(I,J,K,L),K=1,N(I,J)),
     *I=1,NGEN),J=1,NENV)
      IF(IFILE.EQ.1) READ(IVO)(((D(I,J,K,L),K=1,N(I,J)),I=1,NGEN),J=1,NE
     *NV)
   55 CONTINUE
   54 IF(IFAST.EQ.0) GO TO 56
      DO 57 L=1,NVARED
      IF(IFILE.EQ.0.AND.INPUT.EQ.2)READ(5,IFO)(((D(I,J,K,L),K=1,N(I,J)),
     *J=1,NENV),I=1,NGEN)
      IF(IFILE.EQ.0.AND.INPUT.EQ.1)READ(5,/)(((D(I,J,K,L),K=1,N(I,J)),
     *J=1,NENV),I=1,NGEN)
      IF(IFILE.EQ.1) READ(IVO)(((D(I,J,K,L),K=1,N(I,J)),J=1,NENV),I=1,NG
     *EN)
   57 CONTINUE
   56 CONTINUE
      RETURN
      END
```

```
C
C
C     READS INPUT SPECIFICATIONS, LAYOUT OF DATA
C
      SUBROUTINE TWO(NTRAN,NAME,N,D,IFAST,NVARED,NX)
      COMMON /B/NVAR/F/NGEN/L/MAXREP/C/NENV/O/NSUP
      DIMENSION D(NGEN,NENV,MAXREP,NVAR),N(NGEN,NENV),NTRAN(NVAR),IB(74)
     1,IFO(74),NAME(NVAR),NX(80)
      READ(5,1)(NAME(I),I=1,NVAR)
    1 FORMAT(10A6)
   10 A="      "
      DO 50 I=1,74
   50 IB(I)=" "
      READ(5,2) A,(IB(I),I=1,74)
    2 FORMAT(A6,74A1)
      IF(A.IS."FREE") INPUT=1
      IF(A.IS."FREE") GO TO 10
      IF(A.IS."FIXED") INPUT=2
      IF(A.IS."FIXED") GO TO 10
      IF(A.IS."COLUMN") INPUT=3
      IF(A.IS."COLUMN") GO TO 10
      IF(A.EQ."FILE") IVO=3
      IF(A.IS."FILE") IFILE=1
      IF(A.IS."FILE") GO TO 10
      IF(A.IS."FORMAT") GO TO 30
      GO TO 20
   30 DO 51 I=1,74
   51 IFO(I)=IB(I)
      GO TO 10
   20 IF(A.IS."TRANSF") READ(5,/)(NTRAN(I),I=1,NVAR)
      IF(A.IS."TRANSF") GO TO 10
      IF(A.IS."PRINT") NSUP=1
      IF(A.IS."PRINT") GO TO 10
      IF(A.IS."DATA")CALL READE(N,D,IFO,IFILE,IFAST,NVARED,INPUT,IVO,NX)
      IF(A.IS."DATA") RETURN
      WRITE(6,5)
    5 FORMAT(1X,'MISSING DATA CARD;THIS CARD HAS TO BE PRESENT')
      STOP
      END
C
C
C     READS THE UNEQUAL REPLICATES, AND READS READ,DELETE AND NAME CARD
C
      SUBROUTINE ONE(IFAST,NREP,D,N,NTRAN,NAME)
      COMMON /B/NVAR/C/NENV/F/NGEN/L/MAXREP
      DIMENSION D(NGEN,NENV,MAXREP,NVAR),N(NGEN,NENV),NTRAN(NVAR),NAME(N
     1VAR),IB(20),NX(80)
      NVARED=1
      NSCRAP=0
      IF(NREP.EQ.0.AND.IFAST.EQ.1) READ(5,/)((N(I,J),J=1,NENV),I=1,NGEN)
      IF(NREP.EQ.0.AND.IFAST.EQ.0) READ(5,/)((N(I,J),I=1,NGEN),J=1,NENV)
      IF(NREP.GT.0) MAXREP=NREP
      IF(NREP.GT.0) GO TO 10
      MAXREP=0
      DO 50 I=1,NGEN
      DO 50 J=1,NENV
   50 IF(N(I,J).GT.MAXREP) MAXREP=N(I,J)
   10 A="      "
      DO 52 I=1,20
   52 IB(I)=" "
      READ(5,1)A,(IB(I),I=1,20)
    1 FORMAT(A4,20A1)
      IF(A.IS."READ") NVARED=NUMB(IB,20)
      IF(A.IS."READ") GO TO 10
      IF(A.IS."DELE") NSCRAP=NUMB(IB,20)
      IF(A.IS."DELE") READ(5,6)(NX(I),I=1,80)
    6 FORMAT(80I1)
      IF(A.IS."DELE") GO TO 10
      IF(A.IS."NAME") GO TO 30
      GO TO 100
   30 WRITE(6,2) NVARED
    2 FORMAT(1X,'THE NUMBER OF VARIATES TO BE READ IN IS = ',I6)
      NVAR=NVARED-NSCRAP
      IF(NSCRAP.GT.0) WRITE(6,3) NSCRAP
    3 FORMAT(1X,'THE NUMBER OF VARIABLES READ IN BUT DELETED FROM THE AN
     *ALYSIS IS = ',I6)
      WRITE(6,4) NVAR
    4 FORMAT(1X,'THE TOTAL NUMBER OF VARIABLES USED IN THE ANALYSIS IS =
```

```
     *',I6)
      IF(NVAR.LE.1) STOP
      CALL TWO(NTRAN,NAME,N,D,IFAST,NVARED,NX)
      RETURN
  100 WRITE(6,5)
    5 FORMAT(1X,'NAMES CARD IS ABSENT OR IN THE WRONG PLACE')
      STOP
      END
C
C     SUBROUTINE TO CALCULATE PROBALITY THAT F-RATIO GREATER THAN X
C     ARGUMENTS : M IS D.F. FOR TREATMENTS, N IS DF FOR ERROR AND X IS
C                                 CALCULATED  F-RATIO
C
      FUNCTION FISHER(M,N,X)
      IF(X.LE.0.0) GO TO 110
      INTEGER A,B
      A=2*(M/2)-M+2
      B=2*(N/2)-N+2
      W=X*M/FLOAT(N)
      Z=1.0/(1.0+W)
      IF(A.EQ.1.AND.B.EQ.1) P=SQRT(W)
      IF(A.EQ.1.AND.B.EQ.1) D=0.3183098862 *Z/P
      IF(A.EQ.1.AND.B.EQ.1) P=0.6366197724 *ATAN(P)
      IF(A.EQ.1.AND.B.NE.1) P=SQRT(W*Z)
      IF(A.EQ.1.AND.B.NE.1) D=0.5 * P * Z/W
      IF(A.NE.1.AND.B.EQ.1) P=SQRT(Z)
      IF(A.NE.1.AND.B.EQ.1) D=0.5 * Z * P
      IF(A.NE.1.AND.B.EQ.1) P=1-P
      IF(A.NE.1.AND.B.NE.1) D=Z*Z
      IF(A.NE.1.AND.B.NE.1) P=W*Z
      Y=2.0*W/Z
      IF(A .NE. 1) GO TO 90
      IF( B+2 .GT. N)  GO TO 95
      DO 80 J = B+2,N,2
         D =(1.0 + A/FLOAT(J-2))*D*Z
         P = P +D * Y/(J-1)
   80 CONTINUE
      GO TO 95
   90 ZK = Z**((N-1)/2)
      D  = D * ZK * N/B
      P  = P * ZK + W * Z * (ZK -1)/(Z -1)
   95 Y = W * Z
      Z = 2.0/Z
      B = N -2
      IF( A+2 .GT. M)  GO TO 105
      DO 100  I = A+2,M,2
         J = I + B
         D = Y * D * J/FLOAT(I-2)
         P = P - Z * D/J
  100 CONTINUE
  105 IF( P .GT. 1.0)  P = 1.0
      IF(P .LT. 0.0)  P = 0.0
      FISHER = 1 - P
      RETURN
  110 FISHER=1.0
      RETURN
      END
C
C     CALCULARES GENOTYPIC VARIANCE
C
      FUNCTION VG(I,J,XMSG,XMSX,XMSR)
      COMMON /B/NVAR/C/NENV/E/NGDF/H/NXDF,NRDF/K/HARMEN
      DIMENSION XMSX(NVAR,NVAR),XMSR(NVAR,NVAR),XMSG(NVAR,NVAR)
      VG=(1./(NENV*HARMEN))*((HARMEN*HARMEN)*(XMSG(I,I)*XMSG(J,J) +
     1XMSG(I,J)*XMSG(I,J))/(NGDF+2)
     2 + (XMSX(I,I)*XMSX(J,J) + XMSX(I,J)*XMSX(I,J))/(NXDF+2)
     3 + (XMSR(I,I)*XMSR(J,J) + XMSR(I,J)*XMSR(I,J))/(NRDF+2))
      RETURN
      END
```

```
      SUBROUTINE ANOVA(A,NGDF,NEDF,NIDF,NRDF,ZMSG,ZMSE,ZMSI,ZMSR,TOT,EAV
     *E,N)
C
C     THIS SUBROUTINE DOES A TWO WAY ANALYSIS OF VARIANCE
C     USING MATRIX A,      AND UNEQUAL REPLICATES
C
      COMMON /C/NENV/E/NGEN/K/HARMEN/L/MAXREP
      DIMENSION A(NGEN,NENV,MAXREP),TOT(NGEN),N(NGEN,NENV)
      GEN=NGEN
      ENV=NENV
      KMEAN=1
C     THE J DO LOOP
      RECNO=0.0
      SSQE=0.0
      EAVE=0.0
      NO=0
      SSQT=0.0
      TOTAL=0.0
      DO 50 J=1,NENV
        SUME=0.0
        DO 51 I=1,NGEN
          SUM=0.0
          SSQ=0.0
          DO 52 K=1,N(I,J)
            SUM=SUM+A(I,J,K)
            SSQ=SSQ+A(I,J,K)*A(I,J,K)
   52     CONTINUE
          A(I,J,KMEAN)=SUM/FLOAT(N(I,J))
          SSQT=SSQT+SSQ
          TOTAL=TOTAL+SUM
          EAVE=EAVE+A(I,J,KMEAN)
          SUME=SUME+A(I,J,KMEAN)
          NO=NO+N(I,J)
          RECNO=RECNO+1.0/FLOAT(N(I,J))
   51   CONTINUE
        SSQE=SSQE+SUME*SUME/GEN
   50 CONTINUE
C     THE I DO LOOP
      SSQG=0.0
      SSQI=0.0
      DO 53 I=1,NGEN
        SUM=0.0
        DO 54 J=1,NENV
          SUM=SUM+A(I,J,KMEAN)
          SSQI=SSQI + A(I,J,KMEAN)*A(I,J,KMEAN)
   54   CONTINUE
        TOT(I)=SUM
        SSQG=SSQG+SUM*SUM/ENV
   53 CONTINUE
      HARMEN=1./((1./(ENV*GEN))*RECNO)
      CF=EAVE*EAVE/(ENV*GEN)
      SSG=(SSQG-CF)*HARMEN
      SSE=(SSQE-CF)*HARMEN
      SST=(SSQI-SSQG-SSQE+CF)*HARMEN
      SST=SSQT-TOTAL*TOTAL/NO
      SSR=SST-SSI-SSE-SSG
      NGDF=NGEN-1
      NEDF=NENV-1
      NIDF=NGDF*NEDF
      NRDF=NO-1-NGDF-NEDF-NIDF
      ZMSG=SSG/NGDF
      ZMSE=SSE/NEDF
      ZMSI=SST/NIDF
      ZMSR=SSR/NRDF
      RETURN
      END
```

```
C
C     CHANGES A NUMBER IN ARRAY IA IN CHARACTER REPRESENTATION TO NUMBER
C     REPRESENTATION
C
      FUNCTION NUMB(IA,N)
      DIMENSION IA(N),NUMBER(80),NREG(10),NDIGIT(10),IDIGIT(10)
      DATA NDIGIT/'0','1','2','3','4','5','6','7','8','9'/
      DATA IDIGIT/0,1,2,3,4,5,6,7,8,9/
      DO 50 J=1,N
   50 NUMBER(J)=-10
      DO 51 I=1,N
      DO 51 J=1,10
   51 IF(IA(I).EQ.NDIGIT(J)) NUMBER(I)=IDIGIT(J)
      K=0
      DO 52 I=1,N
      IF(NUMBER(I).LT.0.AND.K.EQ.0) GO TO 52
      IF(NUMBER(I).GE.0) K=K+1
      IF(NUMBER(I).GE.0) NREG(K)=NUMBER(I)
      IF(NUMBER(I).GE.0) GO TO 52
      NUMB=0
      DO 53 J=1,K
       NUMB=NUMB+NREG(J)*10**(K-J)
      NREG(J)=0
   53 CONTINUE
      K=0
   52 CONTINUE
      RETURN
      END
C
C     THIS SUBROUTINE TRANSFORMS ARRAY D
C     TRANSFORMATION CODE
C  1=SQUARE ROOT;2=LOG E; 3=LOG 10; 4=1/(1+X); 5=ARCSINE; 6=ARCSINE/100
C
      SUBROUTINE TRANSF(NTRAN,D,N,L)
      COMMON /F/NGEN/C/NENV/L/MAXREP/B/NVAR
      DIMENSION D(NGEN,NENV,MAXREP,NVAR),N(NGEN,NENV)
      IF(NTRAN.LE.0) GO TO 4
      DO 1 K=1,NGEN
       DO 2 I=1,NENV
        IF(N(K,I).LE.0) GO TO 10
        DO 3 J=1,N(K,I)
          IF(NTRAN.EQ.1) D(K,I,J,L)=SQRT(D(K,I,J,L) + 1)
          IF(NTRAN.EQ.2) D(K,I,J,L)=ALOG(D(K,I,J,L) + 1)
          IF(NTRAN.EQ.3) D(K,I,J,L)=ALOG10(D(K,I,J,L) + 1)
          IF(NTRAN.EQ.4) D(K,I,J,L)=1.0/(1.0 + D(K,I,J,L))
          IF(NTRAN.EQ.5) D(K,I,J,L)=ARSIN(D(K,I,J,L))/0.01745329
          IF(NTRAN.EQ.6) D(K,I,J,L)=ARSIN(D(K,I,J,L)/100)/0.01745329
    3   CONTINUE
    2  CONTINUE
    1 CONTINUE
    4 RETURN
   10 WRITE(6,20)
   20 FORMAT(1X,///1X,'ONE OF THE REPLICATE VALUES EQUALS ZERO, THIS IS
     *NOT ALLOWED FOR THIS ANALYSIS')
      STOP
      END
C
C     CALCULATES GENOTYPIC COVARIANCE
C
      FUNCTION COVG(I,J,K,L,XMSG,XMSX,XMSR)
      COMMON /B/NVAR/C/NENV/E/NGDF/K/HARMEN/H/NXDF,NRDF
      DIMENSION XMSG(NVAR,NVAR),XMSX(NVAR,NVAR),XMSR(NVAR,NVAR)
      COVG=(1./(NENV*HARMEN))*((HARMEN*HARMEN)*(XMSG(I,K)*XMSG(J,L)    +
     1XMSG(I,L)*XMSG(J,K))/(NGDF+2)
     3 +(XMSX(I,K)*XMSX(J,L)+XMSX(I,L)*XMSX(J,K))/(NXDF+2)
     4 +(XMSR(I,K)*XMSR(J,L)+XMSR(I,L)*XMSR(J,K))/(NRDF+2))
      RETURN
      END
C
C     CALCULATES PHENOTYPIC COVARIANCE
C
      FUNCTION COVP(I,J,K,L,XMSG)
      COMMON /B/NVAR/E/NGDF
      DIMENSION XMSG(NVAR,NVAR)
      COVP=(XMSG(I,J)*XMSG(K,L)+XMSG(I,K)*XMSG(J,L))/(NGDF+2)
      RETURN
      END
```

TITLE TREELINE CORRELATIONS IN E1 AND E2
****

NUMBER OF GENOTYPES = 27
NUMBER OF ENVIRONMENTS = 2
THERE IS AN UNEQUAL NUMBER OF REPLICATES
FOR READING CARDS: GENOTYPES ITERATE FASTER THAN ENVIRONMENTS
THE NUMBER OF VARIATES TO BE READ IN IS = 28
THE NUMBER OF VARIABLES READ IN BUT DELETED FROM THE ANALYSIS IS = 16
THE TOTAL NUMBER OF VARIABLES USED IN THE ANALYSIS IS = 12

CORRELATION MATRIX: PHENOTYPIC ABOVE DIAGONAL, GENOTYPIC BELOW
****

	HEIGHT	NOFLOW	RHIZ L	RHIZDM	ROOTDM	TOP DM	TOT DM	% RHIZ	% ROOT	% TOP	VEG DM	% VEG
G/X	1.24	0.82	0.94	0.93	1.26	1.17	1.19	0.93	1.00	0.79	1.17	0.53
G/ERROR	2.45	1.61	1.82	1.07	1.79	2.61	2.14	1.64	1.80	1.48	2.71	1.24
X/ERROR	1.98	1.97	1.93	1.29	1.43	2.23	1.80	1.76	1.79	1.89	2.31	2.35
HEIGHT	1.0000	-0.0788	-0.1340	0.0856	0.7761	0.3179	0.5155	-0.1306	0.3849	-0.2649	0.4507	0.1379
NOFLOW	0.0000	1.0000	0.3940	-0.0056	0.0795	0.7682	0.5074	-0.2242	-0.5528	0.7822	0.5610	0.2869
RHIZ L	0.0000	0.0000	1.0000	0.6943	-0.0375	0.4892	0.4734	0.6473	-0.7507	0.1338	0.4938	0.1285
RHIZDM	0.0000	0.0000	0.0000	1.0000	0.1870	0.3193	0.5333	0.8844	-0.5039	-0.3492	0.4280	-0.1223
ROOTDM	0.9182	0.0000	0.0000	0.0000	1.0000	0.5404	0.7659	-0.1152	0.3773	-0.2722	0.6850	0.1665
TOP DM	0.4099	0.0000	0.0000	0.0000	0.9732	1.0000	0.9125	-0.0129	-0.4506	0.4719	0.9415	0.4613
TOT DM	0.4675	0.0000	0.0000	0.0000	0.9907	1.0700	1.0000	0.1810	-0.2701	0.0987	0.9596	0.3185
% RHIZ	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	1.0000	-0.4982	-0.4678	0.0931	-0.2765
% ROOT	6.2233	0.0000	0.0000	0.0000	1.8918	0.0000	0.0000	0.0000	1.0000	-0.5333	-0.3305	-0.2008
% TOP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	1.0000	0.2461	0.4745
VEG DM	0.6919	0.0000	0.0000	0.0000	0.8477	1.1045	1.2080	0.0000	-3.0385	0.0000	1.0000	0.5505
% VEG	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	1.0000

MEAN SQUARE ARRAY FOR GENOTYPES, INTERACTION AND ERROR RESPECTIVELY

	HEIGHT	NOFLOW	RHIZ L	RHIZDM	ROOTDM	TOP DM	TOT DM	% RHIZ	% ROOT	% TOP	VEG DM	% VEG
HEIGHT	0.374	0.014	0.080	0.025	0.317	0.154	0.208	0.008	0.025	0.017	0.196	0.004
HEIGHT	0.302	0.004	0.137	0.060	0.243	0.121	0.175	0.001	0.018	0.017	0.145	0.003
HEIGHT	0.153	0.004	0.005	0.001	0.073	0.039	0.046	0.002	0.004	0.003	0.039	0.002
NOFLOW	0.000	0.085	0.112	0.001	0.015	0.178	0.097	0.007	0.017	0.024	0.116	0.004
NOFLOW	0.000	0.104	0.044	0.012	0.033	0.201	0.121	0.008	0.019	0.027	0.143	0.009
NOFLOW	0.000	0.053	0.005	0.014	0.014	0.080	0.042	0.005	0.007	0.012	0.025	0.003
RHIZ L	0.000	0.000	0.847	0.326	0.024	0.378	0.304	0.065	0.079	0.011	0.342	0.007
RHIZ L	0.000	0.000	1.003	0.395	0.096	0.256	0.311	0.075	0.045	0.030	0.227	0.022
RHIZ L	0.000	0.000	0.521	0.132	0.049	0.048	0.091	0.026	0.013	0.014	0.061	0.007
RHIZDM	0.000	0.000	0.000	0.232	0.060	0.122	0.169	0.044	0.026	0.018	0.147	0.003
RHIZDM	0.000	0.000	0.000	0.279	0.066	0.112	0.183	0.050	0.025	0.024	0.112	0.014
RHIZDM	0.000	0.000	0.000	0.216	0.040	0.041	0.114	0.034	0.014	0.020	0.098	0.003
ROOTDM	0.000	0.000	0.000	0.000	0.447	0.287	0.338	0.008	0.027	0.009	0.326	0.006
ROOTDM	0.000	0.000	0.000	0.000	0.355	0.198	0.259	0.003	0.025	0.022	0.256	0.003
ROOTDM	0.000	0.000	0.000	0.000	0.249	0.127	0.174	0.002	0.021	0.019	0.134	0.008
TOP DM	0.000	0.000	0.000	0.000	0.000	0.631	0.478	0.001	0.039	0.040	0.533	0.019
TOP DM	0.000	0.000	0.000	0.000	0.000	0.540	0.394	0.004	0.042	0.016	0.441	0.022
TOP DM	0.000	0.000	0.000	0.000	0.000	0.242	0.188	0.002	0.011	0.014	0.174	0.000
TOT DM	0.000	0.000	0.000	0.000	0.000	0.000	0.435	0.012	0.019	0.007	0.450	0.011
TOT DM	0.000	0.000	0.000	0.000	0.000	0.000	0.367	0.015	0.022	0.007	0.364	0.007
TOT DM	0.000	0.000	0.000	0.000	0.000	0.000	0.204	0.010	0.003	0.007	0.173	0.004
% RHIZ	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.006	0.005	0.007	0.002
% RHIZ	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.004	0.007	0.002	0.004
% RHIZ	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.003	0.004	0.008	0.000
% ROOT	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.006	0.025	0.001
% ROOT	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.007	0.022	0.001
% ROOT	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.004	0.007	0.001
% TOP	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.018	0.003
% TOP	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.014	0.023	0.005
% TOP	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.001	0.002
VEG DM	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.507	0.021
VEG DM	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.432	0.025
VEG DM	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.187	0.006
% VEG	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003
% VEG	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005
% VEG	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002

SE OF CORRELATION MATRIX
****

	HEIGHT	NOFLOW	RHIZ L	RHIZDM	ROOTDM	TOP DM	TOT DM	% RHIZ	% ROOT	% TOP	VEG DM	% VEG
HEIGHT	0.0000	0.1881	0.1864	0.1879	0.0000	0.1735	0.1422	0.1865	0.1655	0.1785	0.1552	0.1863
NOFLOW	0.0000	0.0000	0.1642	0.1890	0.1881	0.0000	0.1440	0.1816	0.1330	0.0000	0.1307	0.1786
RHIZ L	0.0000	0.0000	0.0000	0.0758	0.1888	0.1479	0.1510	0.1007	0.0000	0.1864	0.1469	0.1866
RHIZDM	0.0000	0.0000	0.0000	0.0000	0.1839	0.1734	0.1380	0.0000	0.1448	0.1790	0.1591	0.1868
ROOTDM	33.9063	0.0000	0.0000	0.0000	0.0000	0.1362	0.0000	0.1871	0.1665	0.1779	0.0815	0.1850
TOP DM	32.0614	0.0000	0.0000	0.0000	35.9872	0.0000	0.0000	0.1890	0.1552	0.1513	0.0000	0.1533
TOT DM	31.2508	0.0000	0.0000	0.0000	36.1356	50.9893	0.0000	0.1842	0.1781	0.1876	0.0000	0.1735
% RHIZ	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1460	0.1521	0.1877	0.1775
% ROOT	********	0.0000	0.0000	0.0000	********	0.0000	0.0000	0.0000	0.0000	0.1380	0.1722	0.1831
% TOP	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1800	0.1508
VEG DM	33.2493	0.0000	0.0000	0.0000	33.7778	53.2943	53.9871	0.0000	********	0.0000	0.0000	0.1336
% VEG	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

SIGNIFICANCE OF CORRELATION MATRIX; BY THE T TEST

	HEIGHT	NOFLOW	RHIZ L	RHIZDM	ROOTDM	TOP DM	TOT DM	% RHIZ	% ROOT	% TOP	VEG DM	% VEG
HEIGHT	NS	NS	NS	NS	NS	(NS)	**	NS	*	NS	**	NS
NOFLOW	NS	NS	*	NS	NS	NS	**	NS	***	NS	***	NS
RHIZ L	NS	NS	NS	***	NS	**	**	***	NS	NS	**	NS
RHIZDM	NS	NS	NS	NS	NS	(NS)	***	NS	**	(NS)	*	NS
ROOTDM	NS	NS	NS	NS	NS	***	NS	NS	*	NS	***	NS
TOP DM	NS	NS	NS	NS	NS	NS	NS	NS	**	**	NS	**
TOT DM	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	(NS)
% RHIZ	NS	NS	NS	NS	NS	NS	NS	NS	**	**	NS	NS
% ROOT	NS	NS	NS	NS	NS	NS	NS	NS	NS	***	(NS)	NS
% TOP	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	**
VEG DM	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	***
% VEG	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS

APPENDIX D

Correlation and Factor Analysis

Correlation of 13 parameters with flowering date, calculated for plants grown on Wakanui soil at Lincoln College only.

	Phenotypic	Genotypic
Plant Height	-.153	-.089
Height : Width Ratio	-.240	-.246
Leaflet Length	.023	.119
Leaflet Length : Width ratio	-.230	-.219
Rhizome Length	.122	.270
Rhizome D.W.	.069	.361
Flower D.W.	.013	-.202
Vegetative Top D.W.	.147	.111
Root D.W.	.159	.158
Total D.W.	.145	.196
Proportion Top	-.092	-.421
Proportion Rhizome	.049	.389
Proportion Root	.038	-.056

Results of Factor Analysis

Variable number	Variable name	Factors 1	2	3	4
1	leaf area	.17	-.14	-.09	-.30
2	leaf length	-.26	.18	.91	.26
3	leaf width	-.53	.19	-.23	-.01
4	leaf length/width	.11	-.09	.73	-.18
5	petiole length	-.57	-.06	.73	-.06
6	height	-.43	-.11	.75	-.13
7	width	-.80	.31	.32	.13
8	height/width	-.03	-.19	.78	-.16
9	Above Ground D.W.	-.87	-.03	-.06	.32
10	Vegetative D.W.	-1.0	.19	.09	.10
1	Root D.W.	-.89	-.26	.27	-.05
12	Total D.W.	-.95	.18	.12	.02
13	Internode length	.03	.20	.53	-.14
14	Number of nodes	.07	.55	-.60	.18
15	Rhizome D.W.	-.45	.84	.06	-.26
16	Proportion rhizome D.W.	.06	.95	.03	-.37
17	Number rhizomes	-.34	.71	-.23	-.33
18	Rhizome length	-.07	.88	.09	-.06
19	Number daughter plants	-.29	.66	.09	-.34
20	Proportion above gd D.W.	.07	-.27	-.17	1.00
21	Proportion vegetative D.W.	-.15	-.40	-.25	.74
22	Flower D.W.	-.02	-.09	-.09	1.00
23	Number of flowers	.00	-.20	-.22	.75
24	Proportion root D.W.	-.12	-.90	.-3	-.21
25	Rhizome branching	-.23	.01	.14	-.14

Correlation Matrix

Phenotypic above diagonal — Genotypic below

	Leaf area	Leaflet length	Leaflet width	Leaflet length-width ratio	Petiole length	Plant height	Plant width	Plant height-width ratio	Above ground dry weight	Proportion above ground D.W.	Vegetative above ground D.W.	Proportion vegetative D.W.	Flower dry weight	Proportion flower D.W.	No. of flowers	Rhizome dry weight	Proportion rhizome D.W.	No. of rhizomes	Rhizome length	No. of nodes	Internode length	Branching of rhizomes	Dry weight/rhizome/length	No. daughter plants	Root dry weight	Proportion root D.W.	Total plant D.W.
Leaf area		-.20	-.26	.00	-.08	-.14	-.29	-.01	-.21	-.01	-.16	.06	-.25	-.08	-.17	-.09	-.04	-.06	-.20	-	-	-	-	.05	-.14	.07	-.18
Leaflet length	-.21		.13	.72	.68	.62	.57	.43	.19	-.37	.42	-.12	.08	.44	-.23	.24	.10	-.08	.25	-.32	.47	.14	.31	.12	.44	.17	.40
Leaflet width	-.27	.07		-.57	.16	.00	.49	-.25	.38	-.12	.50	.14	.08	.23	-.19	.31	.18	.30	.23	.10	.04	.04	.13	.08	.33	-.13	.44
Leaflet length-width ratio	-	.75	-.60		.43	.49	.12	.51	-.12	-.23	.01	-.22	.04	.20	-.06	-.01	-.03	-.25	.06	-.31	-.03	.04	-.03	.05	.11	.22	.01
Petiole length	-.06	.74	.12	.49		.79	.61	.55	.33	-.31	.61	-.02	-.03	.45	-.14	.21	.00	.00	.06	-.21	.19	.18	.16	.10	.62	.26	.53
Plant height	-.11	.65	-	.53	.88		.42	.88	.25	-.34	.42	-.14	-.09	.32	-.13	.17	-.03	.02	-.08	-.38	.17	.24	.14	.21	.55	.31	.45
Plant width	-.30	.63	.53	.14	.73	.46		-.04	.65	-.16	.76	.12	.26	.11	-.03	.49	.17	.28	.35	-.09	.32	.23	.26	.24	.68	-.08	.81
Plant height-width ratio	-	.49	-.29	.57	.65	.92	-		-.06	-.32	.09	-.22	-.21	.29	-.14	-.06	-.09	-.13	-.23	-.33	.39	.09	.15	.10	.25	.37	.08
Above ground dry weight	-.26	.18	.42	-.15	.36	.28	.70	-.03		.41	.97	.46	.47	-.16	.38	.22	-.22	.15	-.03	.05	-.04	.14	.13	.07	.71	-.07	.84
Proportion above ground D.W.	-	.43	-.11	-.27	-.38	-.42	-.11	-.37	.36		.11	.81	.75	.11	.70	-.48	-.58	-.35	-.40	.07	-.26	-.13	-.15	-.40	-.12	-.10	-.10
Vegetative above ground D.W.	-.16	.44	.55	-	.65	.42	.84	.11	.98	-		.39	.34	-.12	.30	.49	-.04	.36	.20	-	-	-	-	.33	.82	-.05	.93
Proportion vegetative D.W.	.08	-.06	.11	-.29	-	-.14	-	-.31	.39	.86	.25		.46	-.04	.50	-.38	-.63	-.33	-.33	-	-	-	-	-.32	.14	.14	.06
Flower dry weight	-.60	-	-	-.60	-	-	.04	.05	.24	1.00	-	.85		-.21	.89	-.17	-.39	-.21	-.11	-	-	-	-	-.17	.09	-.14	.19
Proportion flower D.W.	-.14	.66	.26	-	.70	.51	.12	-.14	-	-.21	-	-.03	-.10		-.27	-.22	-.12	.34	.03	-	-	-	-	-.36	.02	.26	-.15
No. of flowers	-.31	-.29	-.23	-.08	-.15	-.14	-	-.16	.30	.84	-	.68	.78	-.34		-.28	-.41	-.26	-.24	.15	-.11	-.02	-.05	-.25	.00	-.07	.04
Rhizome dry weight	-.07	.26	.34	-.01	.23	.18	.58	-.06	.26	-.55	.65	-.49	-.31	-.19	-.40		.83	.78	.70	.40	.23	.37	.21	.67	.17	-.62	.57
Proportion rhizome D.W.	-.05	.11	.21	-.03	.00	-.03	.19	-.10	-.22	-.61	-	-.66	-.47	-.12	-.50	.85		.70	.79	.45	.23	.19	.07	.60	-.27	-.75	.11
No. of rhizomes	-.05	-.07	.33	-.28	-	-	.32	-.14	.18	-.37	.48	-.43	-.45	-.50	-.35	.85	.78		.52	.36	-.12	.03	-.38	.65	.07	-.57	.40
Length of rhizomes	-.27	.28	.26	.07	.05	-.08	.41	-.29	.00	-.45	.31	-.35	-.14	-	-.35	.74	.84	.54		.66	.42	.06	-.09	.44	-.11	-.64	.22
No. of nodes	-	-.43	.02	-.52	-.51	-.53	-	-.48	-	-	-	-	-	-	.59	.35	.49	.38	.49		-.35	.04	-.12	.09	-.28	-.55	.00
Internode length	-	.62	-	-	.33	.19	.37	.55	-	-.37	-	-	-	-	-.14	.28	.26	-.07	.45	-.56		.02	.01	.04	.07	-.05	.12
Branching of rhizomes	-	.08	-	-	.44	.37	.25	.10	.12	-.20	-	-	-	-	-	.10	.03	-	-	-	-		.45	.35	.18	-.11	.28
Dry weight/rhizome/length	-	.41	.08	.00	.29	.14	.42	.22	.13	-.23	-	-	-	-	-.03	.14	-	-.44	-.05	-.17	-	.63		.14	.24	.04	.28
No. daughter plants	.07	.15	.09	.06	.12	.28	.35	.13	.11	-.53	.44	-.55	-.23	-.64	-.43	.82	.74	.85	.55	.14	-	.18	.10		.09	-.41	.33
Root dry weight	-.14	.46	.33	.12	.70	.61	.74	.27	.75	-.13	.86	.02	-	-	-	.20	-.24	.04	-.13	-.40	-	.27	.33	.12		.43	.86
Proportion root D.W.	-.09	.20	-.15	.26	.31	.38	-.04	.45	-.01	-.04	-.03	.14	-.32	.40	-.04	-.63	-.77	-.67	-.70	-.80	-	-	-	-.52	.46		-.05
Total plant dry weight	-.17	.42	.46	.01	.60	.49	.87	.06	.85	-.06	.95	-	-	-	-	.60	.13	.42	.20	-	-	.27	.38	.45	.88	.00	

APPENDIX E

Data for c.v. Treeline

The 10 columns of data consist of the 2 replicates in 5 environments. Environments in order Wak/low, Cass/low, Wak/Med, Cass/Med, Bealey/high.

Variable names and units are as follows:

ROOTVG - root vigour of transplant, 0-9 scale

TOPVG - shoot vigour at transplanting, 0-9 scale

DATEFL - date of flowering, days from 17th October 1977

LEAFMK - leaf markings, 1 present, blank absent

LEAFAR - leaf area of largest leaf, square centimeters/10

LFLENG - leaflet length, mm

LEWIDT - leaflet width, mm

PETLEN - petiole length, cm

LFWGHT - green weight of leaf, g/100

PETWGT - green petiole weight, g/100

HEIGHT - plant height, cm

WIDTH - plant width, cm

VEG DM - vegetative above ground dry weight g/100

NODAPL - number of daughter plants

NOFLOW - number of flowerheads

FLOWDM - air dry weight of flowerheads, g/100

NORHIZ - number of rhizomes

LERHIZ - length of longest rhizome, cm

RHIZOM - rhizome dry weight, g/100

ROOTDM - root dry weight, g/100

NNODES - number of nodes on longest rhizome

BNODES - number of branching nodes on longest rhizome

VARIETY	TREELINE	GENOTYPE	1							
ROOTVG	3	4	[illegible]	5	5	5	5	[illegible]	[illegible]	4
TOPVIG	4	5	5	7	[illegible]	7	[illegible]	[illegible]	[illegible]	5
DATEFL	58	63	76	81	99	104	134	136	116	
LEAFMK	1	1	1	1	1	1	1	1	1	1
LEAFAR	80	86	120	175						
LFLENG	29	28	36	38	36	30	24	26	17	19
LFWIDT	16	16	18	23	21	19	14	15	14	10
PETLEN	9	6	12	17	8	11	5	5	5	2
LFNGHT	13	17	21	29						
PETWGT	11	10	14	27						
HEIGHT	16	13	11	19	10	11	4	6	4	3
WIDTH	29	27	22	25	14	14	12	17	10	9
VEG DM	1981	1643	292	702	933	677	186	340	106	41
NODAPL	2	2	3	2	1		1			
NOFLOW	163	127	1	21	26	24	1	13	1	
FLOWDM	1652	1384		155						
NORHIZ	5	7	11	6	5		9		2	5
LERHIZ	24	12	44	40	11		26		3	10
RHIZDM	532	30	714	703	16		140	0	4	52
ROOTDM	1169	1460	612	943	628	536	355	614	501	232
ANODES					9		10			
BNODES										

VARIETY	TREELINE	GENOTYPE	2							
ROOTVG	8	6	5	6	5	7	6	5	4	5
TOPVIG	6	4	8	9	9	9	9	9	9	9
DATEFL	81	71	71		128					89
LEAFMK	1	1	1	1	1	1	1	1	1	1
LEAFAR	158	180	73	89						
LFLENG	35	40	22	27	30	34	21	28	18	26
LFWIDT	25	25	18	17	28	23	16	18	13	15
PETLEN	8	14	2	4	5	6	4	3	3	4
LFNGHT	33	31	17	22						
PETWGT	17	33	4	4						
HEIGHT	17	19	3	4	5	9	4	5	5	5
WIDTH	32	28	16	16	13	17	11	13	11	12
VEG DM	2909	2291	390	393	704	679	125	207	132	232
NODAPL	28	12	1	7	3	4	1	1	3	
NOFLOW	60	29	5		3					2
FLOWDM	834	426	16							
NORHIZ	78	45	10	38	13	46	4	10	12	28
LERHIZ	34	36	40	45	19	24	33	33	23	30
RHIZDM	3360	2601	655	1354	886	1217	291	209	353	430
ROOTDM	2459	2759	430	533	321	576	150	424	299	303
ANODES					14	18	18	20		
BNODES					9	12	7	8		

VARIETY	TREELINE	GENOTYPE	3							
ROOTVG	5	2	5	1	5	3	5	6	3	5
TOPVIG	3	3	8	4	3	5	6	7	4	7
DATEFL	51	37	20	120	118	82	130	82		
LEAFMK	1	1	1	1	1	1	1	1	1	1
LEAFAR	100	122	161	110						
LFLENG	27	29	34	28	28	30	24	22	22	20
LFWIDT	20	21	24	22	20	23	19	17	18	14
PETLEN	4	4	4	4	4	4	3	4	3	3
LFNGHT	17	22	28	19						
PETWGT	06	07	10	7						
HEIGHT	5	4	4	3	4	6	3	3	2	4
WIDTH	24	22	18	22	12	10	10	10	9	10
VEG DM	1300	1572	523	400	474	458	216	205	47	58
NODAPL	4	4	2	2					1	
NOFLOW	53	24	11	7	5	7	2	5		
FLOWDM	1538	333	128	53						
NORHIZ	10	28	15	4	6	8	14	8	2	5
LERHIZ	24	26	22	31	17	13	26	20	11	21
RHIZDM	163	578	369	316	101	49	164	66	32	73
ROOTDM	1367	1174	540	358	552	390	286	211	74	122
ANODES					13	13	9	15		
BNODES					2	4	4	3		

VARIETY TREELINE	GENOTYPE 4							
ROOTVG	3	5	4	5	4	3	5	6	1	3
TOPVIG	5	7	9	8	8	6	8	8	5	9
DATEFL	111	71	20							
LEAFMK										
LEAFAR	129	109	109	75						
LFLENG	35	34	33	21	33	35	25	26	26	30
LFWIDT	16	18	17	15	20	17	12	13	11	15
PETLEN	10	10	11	9	10	13	5	6	3	8
LFWGHT	22	25	24	13						
PETWGT	14	16	13	8						
HEIGHT	13	13	13	11	14	10	8	5	5	5
WIDTH	20	30	19	22	16	13	7	12	12	14
VEG DM	1641	2464	580	613	880	491	73	163	67	186
NODAPL	11	21	3	1	1			3		
NOFLOW	1	50	1							
FLODM	9	493	08							
NORHIZ	23	32	8	9	3	20	1	9	5	5
LERHIZ	35	28	35	18	8	14	5	34	10	16
RHIZDM	1784	1130	561	162	87	205	2	273	16	145
ROOTDM	1857	2425	1108	900	1172	803	251	257	182	333
NNODES					7	10	2	12		
BNODES					6	8		4		

VARIETY TREELINE	GENOTYPE 5							
ROOTVG	1	3	4	4	6	1	4	3	9	4
TOPVIG	7	7	9	8	9	6	9	8	9	8
DATEFL	58	71	25		130	125	89		99	15
LEAFMK	1	1	1	1	1	1	1	1	1	3
LEAFAR	144	163	95	165						
LFLENG	36	39	28	35	39	39	20	24	30	24
LFWIDT	22	24	18	25	26	27	12	18	18	14
PETLEN	11	12	9	15	15	11	5	4	5	3
LFWGHT	26	34	18	31						
PETWGT	21	32	11	26						
HEIGHT	14	13	9	13	12	7	4	3	7	6
WIDTH	33	31	20	19	22	18	1	14	12	14
VEG DM	4227	3023	984	651	499	424	185	221	233	499
NODAPL	6	8	6	13	1	2				
NOFLOW	100	63	2		2	2	2		2	15
FLODM	1397	752	15							
NORHIZ	51	44	7	16	4	22	14	8	11	
LERHIZ	31	24	47	51	10	10	23	10	15	
RHIZDM	1463	1109	1884	1517	326	383	155	25	54	
ROOTDM	4892	4407	970	720	1099	1012	511	565	770	536
NNODES					7	8	10	4		
BNODES					5	6	4			

VARIETY TREELINE	GENOTYPE 6							
ROOTVG	3	6	3	3	9	5	6	6	1	3
TOPVIG	5	6	8	9	9	7	9	9	4	8
DATEFL		71	119	75	89	104	134			
LEAFMK										
LEAFAR	101	154	157	117						
LFLENG	30	43	39	33	45	45	25	25	30	32
LFWIDT	19	21	25	21	24	23	15	14	14	15
PETLEN	8	8	11	10	11	10	3	3	4	3
LFWGHT	18	32	28	21						
PETWGT	10	16	17	13						
HEIGHT	10	12	11	9	13	10	5	4	5	6
WIDTH	37	26	26	19	22	20	11	13	10	12
VEG DM	2070	1949	1043	557	1682	1034	127	176	60	123
NODAPL	41	17	5	1		6	1	1	2	
NOFLOW		51	7	21	51	5	1			
FLODM		1068	81	240						
NORHIZ	41	33	15	3		14	7	9	7	6
LERHIZ	35	29	46	45		24	19	17	13	17
RHIZDM	4118	1230	1763	387		790	246	298	68	71
ROOTDM	1122	1982	1103	617	1560	1153	74	379	185	349
NNODES						12	11	5		
BNODES						7	8	4		

VARIETY	TREELINE	GENOTYPE	7									
ROOTVG	2	2	1	7	7	4	3	1	3			
TOPVIG	3	5	6	9	6	8	8	5	9			
DATEFL	78			130	69			136				
LEAFMK	1	1	1	1	1	1	1	1	1			
LEAFAR	102	62	90									
LFLENG	32	26	30	26	47	26	30	25	25			
LFWIDT	17	14	16	15	27	13	16	15	13			
PETLEN	8	7	8	6	15	4	5	6	3			
LFWGHT	26	13	19									
PETWGT	14	15	16	5	12	5	5	6	6			
HEIGHT	7	10	12	14	20	11	13	11	12			
WIDTH	20	23	13	473	1186	130	186	230	173			
VEG DM	691	449	362	1		2	1	1				
NODAPL	13	11	2	2	13			1				
NOFLOW	3											
FLODM	23											
NORHIZ	15	22	14	1	10	10	2	9	4			
LEAHIZ	31	27	29	23	21	20	19	18	17			
RHIZDM	1327	1537	309	526	532	154	244	261	104			
ROOTDM	279	895	780	567	1306	348	343	373	624			
NNODES				5	16	13	9					
BNODES				4	14	4	7					

VARIETY	TREELINE	GENOTYPE	8									
ROOTVG	1	2	4	5	3	5	6	4	4			
TOPVIG	5	5	8	9	8	8	8	6	5			
DATEFL	15	58	35	134	71	99		20				
LEAFMK	1	1	1	1	1	1	1	1	1			
LEAFAR	190	199	109									
LFLENG	42	41	32	31	38	26	24	20	25			
LFWIDT	22	25	20	19	21	17	11	9	15			
PETLEN	10	8	7	10	9	5	3	2	3			
LFWGHT	39	42	23									
PETWGT	23	21	9	8	5	4	4	3	4			
HEIGHT	19	13	5	12	17	13	10	9	9			
WIDTH	42	29	16	781	736	216	133	101	157			
VEG DM	5257	4127	407	2	2	1		1				
NODAPL	5	3	1	2	5	4		1				
NOFLOW	116	93	1									
FLODM	1497	1419	25	17	6	1	5	7	5			
NORHIZ	27	8	12	26	17	28	35	13	22			
LEAHIZ	50	37	55	1256	277	24	131	68	60			
RHIZDM	2389	1152	521	690	769	517	385	385	301			
ROOTDM	3252	3056	457	18	12	12	15					
NNODES				9	9	4						
BNODES												

VARIETY	TREELINE	GENOTYPE	9									
ROOTVG	6	4	4	9	5	2	2	3	3	1		
TOPVIG	5	6	8	8	9	5	8	8	5	5		
DATEFL	71	62			99	134	99	130		136		
LEAFMK	1	1	1	1	1	1	1	1	1	1		
LEAFAR	127	161	258	140								
LFLENG	33	43	53	38	40	38	25	36	36	36		
LFWIDT	21	22	25	21	21	21	16	21	18	20		
PETLEN	12	12	12	5	10	12	4	6	5	9		
LFWGHT	26	39	49	33								
PETWGT	23	30	32	10	9	12	3	7	7	7		
HEIGHT	15	14	15	4	20	20	12	13	12	15		
WIDTH	26	26	19	19	898	644	133	200	145	244		
VEG DM	791	1221	696	280	6	3	1	3	1	2		
NODAPL	12	7	4	3			1	2		1		
NOFLOW	10	7				1	8	9	2	5		
FLODM	272	115				5	27	26	17	22		
NORHIZ	14	15	23	11		12	88	319	43	190		
LEAHIZ	21	21	37	44	840	622	276	215	350	320		
RHIZDM	1204	709	1074	764		4	12	10				
ROOTDM	1467	1921	597	453			9	6				
NNODES												
BNODES												

VARIETY	TREELINE	GENOTYPE	10													
ROOTVG	1	5		9		3		9		4		6		5		3		4
TOPVIG	7	6		8		4		6		8		6		5		4		5
DATEFL	77	85		81		20		60		25		20				20		20
LEAFNK	1	1		1		1		1		1				1				1
LEAFAR	103	222		173		118												
LFLENG	26	51		45		36		50		52		27		33		26		33
LFWIDT	22	25		23		23		25		25		13		14		15		17
PETLEN	7	10		8		8		12		9		3		5		4		3
LFWGHT	26	46		34		24												
PETWGT	15	20		15		9												
HEIGHT	6	18		10		8		10		13		5		5		7		9
WIDTH	26	28		17		14		15		16		10		13		12		14
VEG DM	1596	1826		790		221		669		843		96		127		85		200
NODAPL	19	12		6		1		2		2		1						
NOFLOW	37	9		9		2		1		1				1				3
FLOWDM	568	170		85		38										1		
NORHIZ	40	18		14		8		7		14		3		8		8		7
LERHIZ	31	33		39		37		11		18		22		26		20		18
RHIZDM	1868	2449		1695		963		83		315		32		418		254		103
ROOTDM	889	2031		1186		359		1192		1848		451		264		301		803
NNODES								9		12		12		12				
BNODES								5		6		7						

VARIETY	TREELINE	GENOTYPE	11													
ROOTVG	4			1		3		3		1		2		3		1		3
TOPVIG	4	2		5		7		5		8		4		7		4		5
DATEFL	1	122				119				30		25						104
LEAFNK	1																	
LEAFAR	155	150		135		162												
LFLENG	35	38		41		43		29		35		33		31		40		35
LFWIDT	23	21		21		22		18		19		19		12		18		15
PETLEN	10	9		12		13		11		12		7		4		7		4
LFWGHT	27	34		29		30												
PETWGT	18	18		17		26												
HEIGHT	17	16		12		15		12		7		6		8		7		2
WIDTH	30	20		23		20		14		17		11		7		10		6
VEG DM	2331	756		295		599		261		582		99		49		132		134
NODAPL	24	5		2				4						1				1
NOFLOW	45	2				1				1		1						1
FLOWDM	787	19																
NORHIZ	48	27		9		10		5				5		10				3
LERHIZ	34	23		23		28		14				17		5				17
RHIZDM	2819	655		427		531		124				42		76				75
ROOTDM	2787	1635		544		1290		524		591		298		149		205		237
NNODES								6				6		8				
BNODES								5				5						

VARIETY	TREELINE	GENOTYPE	12													
ROOTVG	1	1		4				2		4		5		5		2		4
TOPVIG	4	5		6				7		6		8		6		5		8
DATEFL	43	71		119				89		118		118		118		118		
LEAFNK																		
LEAFAR	84	78		52														
LFLENG	29	30		23				30		32		22		30		26		20
LFWIDT	18	18		14				19		20		14		17		15		12
PETLEN	8	6		5				9		7		4		5		2		3
LFWGHT	21	22		13														
PETWGT	12	14		4														
HEIGHT	10	13		5				8		6		4		5		6		4
WIDTH	17	17		12				10		13		12		9		11		8
VEG DM	1160	2669				127		201		781		157		157		48		54
NODAPL	15	12		2				1				1		1		1		2
NOFLOW	22	40		1				3		6		2		2		1		
FLOWDM	397	578																
NORHIZ	18	10		8				17		1				10		2		8
LERHIZ	29	22		42				12		6				22		6		33
RHIZDM	1321	204		553				222		4		0		168		17		179
ROOTDM	1605	1141		243				338		961		389		225		280		154
NNODES								10		7				16				
BNODES								7		1				7				

VARIETY	TREELINE	GENOTYPE	13																	
ROOTVG	4	4	3			4	5			3	1			5	5					
TOPVIG	5	6	7			7	5			7	6			7	5					
DATEFL	62	58	93			111	111													
LEAFAK																				
LEAFAR	75	101	87																	
LFLENG	29	30	30			36	34			24	17			34	25					
LFWIDT	17	18	15			23	21			12	12			16	13					
PETLEN	9	10	12			10	10			5	4			3	3					
LFWGHT	15	21	18																	
PETWGT	14	14	11																	
HEIGHT	18	16	10			10	7			5	3			4	6					
WIDTH	29	25	17			13	16			13	10			9	11					
VEG DM	1821	2830	486			444	884			171	136			47	68					
NODAPL	12	14	7			3	2			2	2									
NOFLOW	27	25	2				1													
FLOWDM	435	321	19																	
NORHIZ	39	71	18				5			5	7			2	11					
LERHIZ	26	27	50				15			8	17			11	25					
RHIZDM	1467	1033	575				121			84	216			49	176					
ROOTDM	2266	3034	620			912	1632			356	202			239	162					
NNODES							11			4	11									
BNODES							8			3	8									

VARIETY	TREELINE	GENOTYPE	14																	
ROOTVG	2	1	4	2		3	6			4	3			1	1					
TOPVIG	4	6	6	6		9	9			4	8			5	5					
DATEFL	8	1	75	119		102	99			100				104						
LEAFAK	1	1	1	1		1	1			1	1			1	1					
LEAFAR	140	147	168	149																
LFLENG	39	43	43	40		36	29			27	21			25	24					
LFWIDT	22	20	24	21		22	20			16	15			11	14					
PETLEN	11	12	13	11		12	7			9	5			3	5					
LFWGHT	27	28	31	29																
PETWGT	20	24	25	21																
HEIGHT	20	16	14	12		9	9			5	4			4	4					
WIDTH	30	27	25	16		15	17			11	9			10	10					
VEG DM	2312	2281	878	435		1020	700			164	168			72	68					
NODAPL	11	5	4	1						1										
NOFLOW	33	76	23	3		19	7			1				1						
FLOWDM	470	1336	139	19																
NORHIZ	24	19	6	7						9				5						
LERHIZ	36	32	35	41						31				18						
RHIZDM	3286	1506	1158	392						272	0			58						
ROOTDM	2104	1859	923	579		1303	642			254	486			214	351					
NNODES										15										
BNODES										10										

VARIETY	TREELINE	GENOTYPE	15																	
ROOTVG	1	2	1			6	4				3			3	4					
TOPVIG	2	4	6			7	3			4	8			3	6					
DATEFL	75	71				30									30					
LEAFAK	1	1	1	1		1	1			1	1			1	1					
LEAFAR	151	142	182	117																
LFLENG	43	39	46	33		33	20			33	29			30	40					
LFWIDT	18	21	21	20		19	17			17	15			12	17					
PETLEN	5	8	9	12		9	5			3	4			3	6					
LFWGHT	39	32	38	24																
PETWGT	7	16	15	18																
HEIGHT	9	10	9	10		6	6			7	3			5	6					
WIDTH	25	26	20	17		16	10			9	8			11	12					
VEG DM	641	1253	216	458		483	166			55	75			63	40					
NODAPL	8	12	2	12		1	1								1					
NOFLOW	27	17				4									1					
FLOWDM	315	278																		
NORHIZ	25	20	12	13		2	3			7	5			1	6					
LERHIZ	20	33	42	46		5	10			21	39			19	14					
RHIZDM	519	1511	648	784		71	118			67	118			36	124					
ROOTDM	1304	1079	330	702		813	318			186	249			217	129					
NNODES						6	8			9	17									
BNODES						3	5													

VARIETY	TREELINE	GENOTYPE	16									
ROOTVG	1		5	3	4	7	5	3	1	5		
TOPVIG	5	5	6	6	7	8	9	6	7	9		
DATEFL	1	114		78		126				25		
LEAFMK												
LEAFAR	196	105	201	121								
LFLENG	51	33	46	37	35	39	36	35	36	33		
LFWIDT	23	18	25	19	19	21	19	18	17	15		
PETLEN	14	9	17	14	12	14	4	7	7	3		
LFNGHT	49	24	43	24								
PETNGT	45	14	51	25								
HEIGHT	21	20	19	14	12	14	7	9	6	7		
WIDTH	23	21	21	17	21	13	12	12	7	13		
VEG DM	2182	1696	398	379	226	477	177	162	50	182		
NODAPL	1	5				1		1		1		
NOFLON	79	9		5		3				1		
FLONDM	1069	110		65								
NORHIZ	2	18				3		1				
LERHIZ	25	28				8		7				
RHIZDM	46	806	0	0		26	0	14				
ROOTDM	2334	2346	887	783	529	1121	499	356	158	544		
NNODES						5		6				
BNODES						3		3				

VARIETY	TREELINE	GENOTYPE	17									
ROOTVG	4	3		4	2	3	3	5	4			
TOPVIG	5	3	5	7	5	5	6	9	5			
DATEFL	45	1				91						
LEAFMK	1	1	1	1	1	1	1	1	1			
LEAFAR	105	192	82	172								
LFLENG	35	48	27	42	26	40	21	23	26			
LFWIDT	15	22	16	30	14	21	14	10	14			
PETLEN	8	9	7	13	7	9	7	4	5			
LFNGHT	19	43	17	33								
PETNGT	11	22	7	22								
HEIGHT	13	10	6	16	6	5	4	3	4			
WIDTH	21	18	15	17	9	16	10	13	9			
VEG DM	590	558	171	306	82	334	79	137	107			
NODAPL	17		3		1	1			4			
NOFLON	13	27				5						
FLONDM	380	509										
NORHIZ	10	11	13	6	8	2	11	7	9			
LERHIZ	41	22	32	34	9	6	35	18	12			
RHIZDM	1397	106	586	695	82	12	209	189	279			
ROOTDM	531	678	368	333	260	537	256	452	238			
NNODES					11	4	19	15				
BNODES					7	1	9	8				

VARIETY	TREELINE	GENOTYPE	18									
ROOTVG	9	1	4	1	3	5	4	5	3	3		
TOPVIG	7	9	8	4	9	7	6	9	4	9		
DATEFL	8	1	120	105	111	118	45			20		
LEAFMK												
LEAFAR	167	118	175	172								
LFLENG	42	40	42	46	45	42	38	34	37	30		
LFWIDT	22	18	22	19	23	20	19	15	14	15		
PETLEN	14	11	15	11	16	14	5	5	4	5		
LFNGHT	38	26	39	34								
PETNGT	32	24	34	28								
HEIGHT	24	22	14	15	12	16	6	9	6	6		
WIDTH	28	26	18	21	15	19	14	15	10	12		
VEG DM	2820	2688	947	731	1067	1762	200	340	118	196		
NODAPL	10	13	1	11			1		2			
NOFLON	57	47	3	5	13	18	2			3		
FLONDM	1196	1004	19	83								
NORHIZ	19	24	24	12			12	5	6	3		
LERHIZ	31	33	28	29			22	10	11	3		
RHIZDM	1359	2141	744	1411			91	18	60	4		
ROOTDM	3059	1839	1260	603	1085	1359	328	739	307	451		
NNODES							13	6				
BNODES							3	1				

VARIETY	TREELINE	GENOTYPE	19																	
ROOTVG	2	8	6			5	5	4	6	5										
TOPVIG	7	6	9			8	7	6	9	8										
DATEFL	71	58				99														
LEAFMK			1																	
LEAFAR	104	116	135																	
LFLENG	32	33	33			36	35	27	19	28										
LFWIDT	18	19	21			22	24	17	13	16										
PETLEN	11	5	8			10	12	8	4	4										
LFWGHT	24	22	25																	
PETWGT	19	9	12																	
HEIGHT	11	16	12			6	10	7	4	6										
WIDTH	33	22	22			23	19	12	13	12										
VEG DM	1741	1186	924			1900	401	148	152	101										
NODAPL	5	17	21			1	3		3											
NOFLOW	75	4				47														
FLOWDM	1342	66																		
NORHIZ	20	55	23			5	7	8	8	4										
LERHIZ	22	24	40			10	7	27	13	14										
RHIZDM	507	873	2570			92	108	197	177	24										
ROOTDM	1718	3215	995			1248	883	325	388	473										
NNODES						8	7	13	9											
BNODES						5	4	11	4											

VARIETY	TREELINE	GENOTYPE	20																	
ROOTVG	7	6	3			9	5	7	9	5	7									
TOPVIG	6	7	6			7	7	7	6	4	7									
DATEFL	47	1	25			130	104	118	45		15									
LEAFMK	1	1	1			1	1	1	1	1	1									
LEAFAR	184	118	129																	
LFLENG	44	36	36			37	40	34	37	34	33									
LFWIDT	22	18	19			19	21	17	18	14	16									
PETLEN	11	7	9			8	12	4	6	5	5									
LFWGHT	42	28	24																	
PETWGT	24	13	13																	
HEIGHT	11	10	7			4	8	5	5	5	5									
WIDTH	28	21	20			17	18	14	13	13	13									
VEG DM	1791	748	403			317	485	133	135	90	145									
NODAPL	17	2	2						4		1									
NOFLOW	20	11	1			5	8	2	1		1									
FLOWDM	379	256	16																	
NORHIZ	21	12	12			5	11	7	6	5	8									
LERHIZ	37	32	44			17	21	33	34	29	23									
RHIZDM	2746	944	726			332	273	183	433	262	95									
ROOTDM	1456	980	879			593	802	309	127	144	552									
NNODES						7	10	13	16											
BNODES							4	2												

VARIETY	TREELINE	GENOTYPE	21																	
ROOTVG	1	1	6	1		3	5	4	3	5	5									
TOPVIG	3	7	9	7		7	8	6	8	7	7									
DATEFL	64	8	51	105		99	71	71	61	25	51									
LEAFMK	1	1	1	1		1	1	1	1	1	1									
LEAFAR	202	126	192	135																
LFLENG	43	33	42	34		30	28	26	19	25	27									
LFWIDT	26	21	27	24		20	20	16	17	15	15									
PETLEN	11	8	11	9		9	6	4	3	5	2									
LFWGHT	43	31	44	27																
PETWGT	18	13	21	12																
HEIGHT	20	13	12	10		10	6	5	4	5	4									
WIDTH	27	24	22	18		15	14	11	8	11	12									
VEG DM	3200	1470	285	598		740	617	127	133	163	140									
NODAPL	10	11	2			2	1				1									
NOFLOW	53	48	3	5		24	11	2	4	4	2									
FLOWDM	856	799	15	44																
NORHIZ	25	16	1	11		5	1	4			2									
LERHIZ	29	34	17	46		20	17	31			21									
RHIZDM	1316	1713	7	888		218	272	213	0		74									
ROOTDM	4136	2326	848	793		537	684	249	236	356	395									
NNODES						14	11	10												
BNODES						12	10	8												

VARIETY	TREELINE	GENOTYPE	22																	
ROOTVG	1	1		3		1		1		3		4		4		3		4		
TOPVIG	6	7		5		9		5		7		9		7		8		9		
DATEFL	83	107				25		118		104		35				30				
LEAFMK	1	1		1		1		1		1		1		1		1		1		
LEAFAR	218	226		246		111														
LFLENG	46	48		50		31		29		42		30		32		24		22		
LFWIDT	28	28		27		21		20		25		17		20		12		13		
PETLEN	13	15		14		11		6		11		5		5		2		3		
LFWGHT	53	48		47		20														
PETWGT	36	40		36		16														
HEIGHT	20	20		18		12		8		14		5		5		5		5		
WIDTH	30	29		23		18		10		15		6		12		13		8		
VEG DM	3435	2787		639		583		330		1501		57		144		103		44		
NODAPL	6	5		1		1								1		1				
NOFLOW	89	15				6		7		23		1				1				
FLOWDM	1221	176				77														
NORHIZ	17	28		12		5				3				5						
LERHIZ	21	18		31		35				10				14						
RHIZDM	714	728		370		179				23		0		18						
ROOTDM	3870	3550		1272		1172		304		1853		209		325		372		233		
NNODES										7				6						
BNODES										1										

VARIETY	TREELINE	GENOTYPE	23																	
ROOTVG	1	8		1				3				4				2				
TOPVIG	8	8		9				5				7				6				
DATEFL	75	50		25				118												
LEAFMK																				
LEAFAR	225	222		199																
LFLENG	52	51		41				27				27				30				
LFWIDT	24	24		26				16				18				17				
PETLEN	10	10		13				6				6				3				
LFWGHT	42	41		27																
PETWGT	26	27		20																
HEIGHT	14	16		12				7				6				5				
WIDTH	33	20		26				12				14				14				
VEG DM	2838	488		589				291				152				108				
NODAPL	11	1		4								1				2				
NOFLOW	92	1		4				8												
FLOWDM	1805	1		69																
NORHIZ	38	7		8								5				7				
LERHIZ	24	16		47								37				24				
RHIZDM	1553	222		1344								411				328				
ROOTDM	2660	866		751				503				210				348				
NNODES												11								
BNODES												9								

VARIETY	TREELINE	GENOTYPE	24																	
ROOTVG	3	4		1		3		3		2		4		5		5		4		
TOPVIG	4	4		5		7		8		4		6		9		7		7		
DATEFL	58	58		109		71		111		118		35		71		20		134		
LEAFMK	1	1		1		1		1		1		1		1		1		1		
LEAFAR	120	132		117		111														
LFLENG	32	36		32		30		48		52		32		28		27		29		
LFWIDT	20	20		16		18		28		27		16		17		14		15		
PETLEN	9	10		8		11		18		16		6		5		3		6		
LFWGHT	21	24		25		20														
PETWGT	12	14		10		13														
HEIGHT	12	10		9		11		17		15		7		4		6		7		
WIDTH	32	28		15		15		17		16		8		12		13		11		
VEG DM	1537	1512		205		373		523		380		89		216		118		177		
NODAPL	9	20				12										1				
NOFLOW	64	60		1		4		10		5		1		4		1		2		
FLOWDM	961	1054				24														
NORHIZ	32	24		3		20		4		3		5		1		9		4		
LERHIZ	32	20		33		45		28		17		31		11		8		16		
RHIZDM	1952	619		64		1749		239		78		109		39		22		24		
ROOTDM	1722	1781		556		263		772		607		245		456		360		396		
NNODES								14		9		11		5						
BNODES								10		5				3						

VARIETY	TREELINE	GENOTYPE	25									
ROOTVG	1		2	1	2	2	1	3	1	1		
TOPVIG	6	4	9	9	8	8	9	9	5	6		
DATEFL	81	51		97	122	111						
LEAFMK	1	1	1	1	1	1	1	1	1	1		
LEAFAR	92	101	95	81								
LFLENG	29	32	28	28	37	39	30	26	32	25		
LFWIDT	16	18	19	17	22	19	19	13	15	14		
PETLEN	6	5	9	6	10	4	7	5	4	3		
LFWGHT	16	23	21	17								
PETWGT	08	08	14	7								
HEIGHT	8	7	8	4	10	9	8	6	5	5		
WIDTH	26	25	22	22	17	14	9	8	11	11		
VEG DM	1033	355	366	419	351	337	149	72	62	59		
NODAPL	11	15	4	13	2	1	1	1	3	2		
NOFLOW	6	8		1	2	4						
FLOWDM	192	304										
NORHIZ	30	25	12	24	16	18	8	4	5	6		
LERHIZ	33	25	20	35	20	12	23	13	24	19		
RHIZDM	1890	1127	183	487	413	413	131	244	192	199		
ROOTDM	1480	688	664	668	791	531	320	146	104	153		
NNODES					9	10	11	11				
BNODES					9	7	7	5				

VARIETY	TREELINE	GENOTYPE	26									
ROOTVG	2		5	7	4	6	6		6	5		
TOPVIG	7	2	9	8	7	9	9		7	9		
DATEFL	1	125	25	35	37	35	40		111	25		
LEAFMK												
LEAFAR	186	112	175	238								
LFLENG	44	36	43	53	42	31	39		39	27		
LFWIDT	26	19	22	26	19	19	24		18	18		
PETLEN	10	10	16	16	7	9	7		5	3		
LFWGHT	46	32	37	53								
PETWGT	31	20	41	51								
HEIGHT	24	20	18	15	10	10	7		7	7		
WIDTH	24	24	20	13	11	13	15		15	13		
VEG DM	1868	670	864	615	698	643	382		219	251		
NODAPL	1											
NOFLOW	14	1	8	2	6	13	9		2	1		
FLOWDM	55	13	66	15								
NORHIZ	17	4	3	4								
LERHIZ	21	16	13	18								
RHIZDM	245	32	16	41			0					
ROOTDM	2000	1154	1741	1630	913	831	707		510	472		
NNODES												
BNODES												

VARIETY	TREELINE	GENOTYPE	27									
ROOTVG	2	2	3	1	3	3	3	2	1	1		
TOPVIG	6	5	9	6	4	7	7	4	4	5		
DATEFL	88	71	109	119		118			51			
LEAFMK	1	1	1	1	1	1	1	1	1	1		
LEAFAR	74	92	111	142								
LFLENG	27	30	31	36	30	32	24	24	32	25		
LFWIDT	16	18	19	20	18	18	13	12	19	12		
PETLEN	10	11	12	12	10	10	7	5	4	3		
LFWGHT	15	20	24	25								
PETWGT	13	17	18	22								
HEIGHT	16	16	12	14	10	9	6	4	7	4		
WIDTH	26	27	18	19	10	16	9	10	15	10		
VEG DM	1417	1523	770	658	457	608	109	161	145	87		
NODAPL	16	3			1	1	1					
NOFLOW	3	8	10	7		2			1			
FLOWDM	31	97	90	56								
NORHIZ	29	38	11		16	2	8		2	1		
LERHIZ	19	26	13		7	7	16		11	6		
RHIZDM	1232	1234	22	0	63	30	106	0	77	13		
ROOTDM	2641	3170	1481	1732	1114	1323	257	466	515	313		
NNODES					7	4	6					
BNODES					3	4	5					

APPENDIX F

Visual scores and winter survival at site six.

Site six was situated at 1200 m a.s.l. approximately 500 m from the high altitude site of Experiment One. The soil in site six was transported to it and was Wakanui Silt Loam. It was in every respect established in a similar manner to the other five sites.

The plants at this site were not harvested in March 1978 as the plants had been grazed by hares and alpine grasshoppers.

On 11 December 1978 the plants were scored for survival and their size accessed on a 0-9 scale. Plants with 0 were alive but with only one leaf while plants with 9 had about 30 leaves. The results were:

		Mean Score	Survival (%)
Forest	2x	1.6 c	88
Summit	2x	1.6 c	97
51140	4x	1.7 c	73
Treeline	4x	2.3 b	78
57353	6x	4.0 a	90
Prairie	6x	4.1 a	90
Huia		not measured	77 (10/13)
Maku		not measured	38 (5/13)

The high survival rates of all *T. ambiguum* varieties was unexpected. It was expected that a large number of plants would have been killed through frost heave, especially the poorly adapted plants. It was interesting to note that Maku had a lower survival rate but because of the low number of plants involved this may not be a significant effect. The relatively high fertility soil conditions probably allowed the plants to survive the harsh climatic conditions. It would have been very unlikely to obtain such high

survival rates in soil native to the area.

The larger size of the hexaploid plants was unexpected as these were expected to be poorly adapted to high altitude conditions. Perhaps the previous seasons rhizome production, which would have been greater than the diploids and tetraploids, gave the plants sufficient reserves to produce some spring growth. Another reason may be that the hexaploid plants contained large amounts of cyanogenetic glucoside (Portz, 1955) and were therefore not grazed as hard by alpine grasshoppers in the previous season. This would have allowed the plants to establish themselves more than grazed plants and consequently have an advantage in spring. It is also known that some tetraploid plants contain cyanogenetic glucoside while the diploids do not contain any (Currier pers. com.). If cynanogenetic glucosides prevent grazing by alpine grasshoppers then this would have important consequences for the future use of *T. ambiguum* for high country revegetation work.